

Table 70: Comparative Sequences relating to SAG 1280

ATACCTTTATTGAGTTTGAAACCTTGGAAATTGATTTCTTTTGTGGATGAGGCTCATC
 ACTTCAAGAAATATCCGTCCAATCACTGGACTTGGGAATGTAGCTGGAATCACCACACAA
 CTTCTAAAAAGAACGTTGGATATGGAGATGAAGGTGAGACAGTACAGGCAGAGCATGGAG
 ATAGAAATGTCTGTTTTCGCGACAGGAACACCAAGTTTCTAACTCTATTAGTGAACCTTTCA
 CCATGATGGATTACATTTCAACCTGATGTCTTGGAACGATACCTGGTATCAAAATTTGACT
 CCTGGGTTGGGGCTTTTGGGAATATCGAAACTCCATGGAAGTACCCCGACAGGAGATA
 AGTACCAACCCAGAAACGTTCAAGAAATTTGTCAACCTTCCTGAACTCATGCGAATCT
 ACAAGGAACTGCCGATATTAGACCTCAGACATGCTTGATTTACCAGTACCGGAAGCTA
 AGATTATTGCGGTGGAAGCGAGTTAACGCAAGCTCAGAAATCTATTGGAAGAGCTGG
 TAAAGCGTTGAGACGCTATCAAGTCAGGTAGTGTGATCCAAGTAGAGATAACATGCTTA
 AAATCACAGGAGAAGCCAGAAACTAGCTATTGATATGCGGTTGATTGACCTACTTACT
 CCTTATCGGATTAATCAGAAATCCTTCAAGTAGTTCGATAATGTGCGAGCGGATTACCGTG
 ATGGAGCTGGAGACAAGCCACTCAGATGATTTCTCAGATATTGGAACCCCTAAAGTA
 AGGAAGAAGGGTTTGATGTCTACAATGAACCTTAAGGACTTGTTTGTGCGATCGAGGGATAC
 CAAAGAGAGAAATTTGCTTCCATGATGCCAATCTGATGAGAAGAAAACTCTCTGT
 CAGCAAGGTCAATAGTGGAGAAAGTACGGATTCTCATGGCTTCTACGGAAGGAGGGGAA
 CAGGATTAAACGTTCAATCTCGCATGAAAGCTGTCCACTATTAGACGTTCCCTGGAGGC
 CCTCAGACATTTGTCAGCGAAATGGACGACTAATTCGACAAGGAAACATGCACCGAGG
 TAGATATTATCACTAATATTACTAAAGGGAGCTTTGACAATTACCTCTGGCAGACGCGAG
 AGAATAAGCTAAAGTATATCACCAGATAATGACCTCAAAGATCCTGTGAGATCAGCTG
 AAGACATTGATGAACAAACCATGACCGCTCAGACTTTAAGGCATTGGCAACTGGGAACC
 CTTATCTCAAACCTCAAATGGAGTTGGAAATGAACCTGACAGTTTATAGAGAACTCAAAC
 GAGCCTTTAATCGCTCCAAAGACGAGTATCGCCATACCATTTCTATAGCGAGAAGCACC
 TCCTTATTATGGAAACCGTTGAGTCAATATGATAAAGATATTGCCCAATCTTTGGCAA
 CCAAGTCGCAAGATTGTTGTCATGCGATTGACAATCAAGCAATGGATAATCGTGCTGAAG
 CTGGGGACTATCTGCGAAACCTATTACCTATAACCGCTCAGAGACCAAGGAAGTCAGGA
 CACTTGGCAGCTTTAGAGGATTTGATTTAAAAATGACTACACGAGGTGCTAGTGAGCCCT
 TACCAGAAACCATTTCTTAAATGATTGATGGTATGATACAGTATCTGTCGCCCTTGATT
 TGAATATCAGACCTGGGAACCATTTCAACGATTAGTAATGCCATTGACCATATTATAGATG
 ACCAAGAAAGACGCAAGAGCTGGTAAAGGATTTAAAGATAAGCTACAGTAGCCAAAG
 TAGAAGTTGATAAAGTCTTTCCAAAGGAAGAGGACTATCAGCTTGTAAGGCTAAGTATG
 ATGTTTATGCTCCCTTGGTTGAAAAGAGAGCAGAGATTGAAGAGATAGATGCAGCTTTGG
 CCAAGTTTAGTGAAGATACAAACCCCAAGGAAGCAACAAATAGCAGCTCGAGATA

SEQ ID. NO. 7002

STRAIN H36B

GGAGGGAAAAATGAATCAAGAAGTCTTACTACAAATGAT
 GAGAGCCACTATTCCTCGTATAGAGCCCTTGCTTGAGGCATTTTATATT
 ACCAAGCAGAGCATTTTGATGAGGAGTGGGATAGTCTTATTCATCAGTTT
 ATGACCAATAGGCAAGAAATAAATAAGTCTGTTCAAGTACTTCACTTTGA
 GACAGATGTTTCAAGCTTTTGTCCAGGCTAGTCTTATGATAGTCTCATG
 ATCTATTGACCTATACACAAGTTTTCGGCCAAAGTGGTCTTCAAAAACTA
 GATAAATATCGCCGCTCGAAAAAACTTGGTGATAGAAGTGGCCTTGT
 CAATCTGGCCACTCGTTTCAATATTGGATTCCAATGGACACTACCAA
 CCATATCGCCGATTCACTCTTACAAAAGAGTAGGGAGCTAATTTGGTC
 AATGTGTATCGTGTGGCTAATAATTAGCGGATCGTATTAGTTCGAGATAT
 TGAACAGTTTCTCTTAACCTACGAGCCTGAGCTTGAACTAGAGCTGATG
 AAAGTGTCTAGAAAAATGAAGAACTGTTGATGAGCAGCAAAAACAGTGTT
 CATCAAGCAATATCTTTGAGAGAGAGGGCTCTCTGTTATTGCTAGTTT
 GGATGTAGATTGTTCTCAACTAGATGTTCAAAATAGGAAAAACAGTCATC
 TGCCAGCTTATGAAGAGTTATCCTTACGACGTAATTTGAGATTCTAACA
 TATTTTGACCAAAATCGAAATGAACGTTCCAAAGTCCCAAGTTTATAGAG
 AGGTGATTTTGACACAGAGATGGAAATGACACAGTCTTTGATGGCGAGG
 AATTACTTACTTATCTCGAAGCTGATGGCAGTCCCTATGAGCTGAAACGA
 ACGCTGACTACAGTCAAGAAAAAGGAATTAGAAAAAATGGACAAAGCCAT
 TAGGATAGAAAAATCAAGAAAAATGACTCAGCTA₅GkATTGrTTTATCTC
 AGTTTGACCCAGACCGAGTGGTATTTTATTGKATGAGCAGGTCGTYyT
 CGTTTawAwAATGCAGACCTTGCTTCACTAGGTGGTTATCCAAAGCCTC
 GGTAACTCAACTAGCCCTTGCGACAGAACTACTCCAAATGGGACTAAGTC
 ATGAAAAGGTTGAATTTTCTTTGGTAGCCAGCTTCCATGGAAGAGCTG
 CGACAAGTTGCTACGCCCTTTTACACCAAGAACTCAGCAGAGAGATGC
 GGAGCAATTTGAAAAAGATAAAGGTAATCAGCCAGATTAACTCTCAGAG
 ATTGGAAGCAAGCTAGAGAAAGCTGAGGGAAAAGAGTAGTTGATGAA
 GAATTCGCGGAAAATCCACTGGTTAGAGAGTATTGGACACTTATCCTCT
 GGGGTCAITGGTTTCTATAAGGGACAGGACTTTGAGGTCATGTGCGTCA
 GCGATGCTCGATGAACGGTTTGATTGCGATTGAGTTAGTCAATGACTTT
 TCGGATATCATTGAACAAAATCCAGTTCTTTATGTGAGGACCTGGGAAGA
 AGTCAGTCAGGCACTTCATCAGCCAAAGGCAGAACCAAAACAGAGTTAG
 AAGAAGCGGACCAAGAATTAAACCTATTCTCATTTCTGGAAGAGGAGCTA
 GTTCAGAGTATTGGACTATTGGAACAGATGATTAGAAAAATGGTCATAA
 CGATACTGATCTTGAAGAAAACAGATAATCAAAATTCCTGAAGAGGAAGTCG
 TCGAAACAAATCCAGAGATTCCAGTAAACGGACTTTTATTTCCAGAAGAT
 TTGACGGACTTTTATCCTAAGACTGCTAGAGATAAGTTGAGACAAACAT
 TGTGGCCATTCTTTGGTAAAAATCTAGAAGTAGAGCACCGCAATGCTT
 CACCAAGTGAACAAAGAACTCTTGCCAAGTATGTAGGCTGGGGTGGACTA
 GCCAATGAATTTTGTGACTATAATCCAAATTTTCTAAGGAACGAGA
 AGAAGTGAAGAGCTAGTCACAGATAAAGAGTATTGCGATATGAACAGT
 CCTCCTGACAGCCTATTACACAGACCCATCCCTGATCCGTGAGATGTGG
 GATAAGTTGGAAGAGATGGCTTTACAGGTGGCAAAATCCTAGATCCTTC
 CATGGGAACAGGGAATTTCTTTGCGGCTATGCCAAAACACTTAAGAGAAA
 AGAGTGAGTTGATGGCGTAGAGTTAGATACTATTACAGGAGCTATTGCC
 AAACACCTTCATCCCAATAGTCATATTGAATTAAGGGATTTGAGACGGT
 GGCTTTTAAACGCAATAGTTTGGATTGGTGATTCAAATGTGCCCTTTG

Table 70: Comparative Sequences relating to SAG 1280

CCAATATACGAATTGCGGATAATAGGTACGATAGGCCCTTACATGATTTCAT
 GACTACTTTGTCAAAAAGTCACTTGATTGCTTCATGATGGTGGACAAGT
 AGCGATTATCTCTTCCACAGGAACATGATAGGATAAGCGAACAGAAAACATCT
 TACAAGATATTCTGTAGACAACCTGAATTTCTTGGTGGGGTTCGACTGCCT
 GACTCTGCCCTTAAGGCCATTGCGAGAACGAGTGTCAACACGGATATGTT
 ATTCTTCCAGAAACACTTAGACAAGGGATATGTGGCAGACGATTTAGCCCT
 TTTGAGTTCCATTTCGTATGACAAGGATAGTCGCATTTGGCTCAATCCT
 TATTTTGATGGAGAATACAATAGCCAGGTGCTAGGAACCTACGAGGTGAG
 GAATTTTAACGGAGGAACACTTTCTGTTAAGGGGACTAGTGATGACTTGA
 TTGCAAGTGTGAAACAGCTCTAAATCACGTTAAGGCCCAAGAGAGATT
 GATAGAAATGAGGTCACTTAACCCAGATGTGTTGACCAACCAAGTCAA
 TGATACCTCCATTCCAGCTGAAATGAGGGAAAATCTAGGTGAGTACAGTT
 TTGGTTATCAGGGGTCTACAGTTTACTATCGAGATAACAAAGGCATTTCGA
 GTCGGAACCAAGACGGAAGAAATCAGTTACTATGTCGATGAAGAG

SEQ ID. NO. 7003

STRAIN 18RS21

GnAGGGAAAATGAATCAAGAAGTCTTACTACAAATGATGAGA
 GCCACTATTCTCGTGATAGAGCCTTGCTTGAGGCATTTTATATTACCA
 AGCAGAGCATTGATGAGGAGTGGGATAGTCTTATTTCATCAGTTTATGA
 CCAATAGGCAAGAAAATAAATAGTCTGTTCAAGTACTTCACTTTGAGACA
 GATGTTTCAGCTTTTGTCCAGGCTAGTCTTATGATACTGCTCATGATCT
 ATTGACCTATACACAAGTTTTCGGCCAAAGTGGTCTTCAAAAACCTAGATA
 AACTATCGCCGCTGAAAAAACTTGGTGATAGAAGTGGCCTTGTTCAT
 CTGGCCACTCGTTTCAATTATTTGGATTCCAAATGGACACTACCAACCAT
 ATCGCCGATTCACTCTTACAAAAGAGTAGGGGAGCTAATTTGGTCAATG
 TGTATCGTGTGGCTAATAATTTAGCGGATCGTATTAGTCGAGATATTGAA
 CAGTTTCTCTTAACCTTACGAGCCTGAGCTTGAAACTAGAGCTGATGAAAC
 TGTCTAGAAAAATGAAGAACTGTTGATGAGCACAACAAAGTGTTCATC
 AAGCAATATCTTTTCGAGAAGAGGGCTCTCTGGTTATTTGCTAGTTTGGAT
 GTAGATTTGTCTCACTAGATGTTCAAATAGGAAAAACAGTCATCTGCC
 AGCTTATGAAGAGTTATCCTTACGAGCTAAATTTGAGATTCTAACATATT
 TTGACCAAAATCGAAATGAACGTTCCAAAGTCCCAAGTTTGTAGCAGGTT
 GATTTTGACACAGAGATGGAATGACACCAAGTCTTGTATGGCGAGGAATT
 ACTTACTTATCTCGAAGCTGATGGCAGTCCCTATGAGCTGAAACGAACGC
 TGACTACAGTcGAAGAAAAGGAATTAGAAAAAATTTGGACAAGCCATTAGG
 ATAGAAAAATCAAGAAAAATGACTCAGCTAGGGATTGATTTATCTCAGTT
 TGACCCAGACCGAGTCCGTTATTTTATTTGGATGACAGCGGTCTTTTCGTT
 TAAAAAATGACAGCCTTGCTTTACTAGGTGGTTATCCCAAAGCCTCGGTA
 ACTCAACTAGCCCTTGGCAGACAGAACTACTCCAATGGGACTAAGTCATGA
 AAAGGTTGAATTTTCTTTGGTAGCCAGCTTTCCATTGAAGAGCTGCGAC
 AAGTTGCCCTACGCCCTTTTACACCAAGAACTCAGCAGAGAAGATGCGGAG
 CAATTTGAAAAAGATAAAGGTAATCAGCCAGATTAACTCTCAGAGATTG
 GAAAGCAAGCTAGAGAAAGCTGAGGGAAAAGAGTAGTTGATGAAGAAT
 TCGCGGAAAATCCACTGTTTCCAGAGATTTGGACACTTATCTCTGGGG
 TCATTGGTTTCTTATAAGGGACAGGACTTTGAGGTCAATGTCGGTTCAGCGA
 TGCTCGATTGAACGGTTTGATTTCGGATTGAGTTAGTCAATGACTTTTCG
 ATATCATTGAACAAAAATCCAGTTCTTATGTGAGGACCTGGGAAGAAAGTC
 AGTCAGGCACTTCATCAGCCAAAGGCAGAACCAACAAAGAGTTAGAAGA
 AGCGGACCAAGAATTAAACCTATTCTCATTCTGGAAGAGGAGCCAGTTT
 AGAGTATTGGGACTATTGGAACAGATGATTGAGAAATGGTTCATAACGAT
 ACTGATCTTGAAGAAACAGATAATCAAATTCCTGAAGAGGAAGTCTGCGA
 AACAAATCCAGAGATTCCAGTAACGGACTTTTATTTTCCAGAAGATTGA
 CGGACTTTTATCTTAAGACTGCTAGAGATAAGGTTGAGACAAACATTGTG
 GCCATTCTGTTGGTAAAAAATCTAGAAGTAGAGCACCAGCAATGCTTCACC
 AAGTGAAACAGAACTCCTTGCCAAGTATGTAGGCTGGGGTGGACTAGCCA
 ATGATTTTGTGATGACTATAATCCAAAATTTTCTAAGGAACGAGAAGAA
 CTGAAGAGCCTAGTCAAGATAAAGAGTATTCCGATATGAACAGTCCCTC
 CCTGACAGCCTATTACACAGACCCATCCCTGATCCGTGAGATGTGGGATA
 AGTTGGAAGAGATGGCTTTACAGGTGGCAAAATCCTAGATCCTTCCATG
 GGAACAGGGAATTTCTTGGCGCTATGCCAAAACACTTAAGAGAAAAGAG
 TGAGTTGTATGGCGTAGAGTTAGATACTATTACAGGAGCTATTGCCAAAC
 ACCTTTCATCCCAATAGTCATATTGAAATTAAGGGATTGAGACGGTGGCT
 TTTAACGACAATAGTTTGAATTTGGTGATTTCAAATGTGCCCTTTTGCCAA
 TATACGAATTGCGGATAATAGGTACGATAGGCCCTTACATGATTTCATGACT
 ACTTTGTCAAAAAGTCACTTGATTGCTTTCATGATGGTGGACAAGTAGCG
 ATTATCTCTTCCACAGGAACCTATGGATAAGCGAACAGAAAACATCTTACA
 AGATATTCTGTAGACAACCTGAATTTCTTGGTGGGGTTCGACTGCCCTGACT
 CTGCCCTTAAGGCCATTGCGAGAACGAGTGTCAACACGGATATGTTATTTC
 TTCCAGAAACACTTAGACAAGGGATATGTGGCAGACGATTTAGCCCTTTTC
 AGGTTCCATTTCGTATGACAAGGATAGTCGCATTTGGCTCAATCTTATT
 TTGATGGAGAATACAATAGCCAGGTGCTAGGAACCTACGAGGTGAGGAAT
 TTTAACGGAGGAACACTTTCTGTTAAGGGGACTAGTGATGACTTGATGTC
 AAGTGTGAAACAGCTCTAAATCACGTTAAGGCCCAAGAGAGATTGATA
 GAAATGAGGTCACTTAACCCAGATGTGTTGACCAACCAAGTCAATGAT
 ACCTCCATTCCAGCTGAAATGAGGGAAAATCTAGGTGAGTACAGTTTGG
 TTATCAGGGGTCTACAGTTTACTATCGAGATAACAAAGGCATTTCGAGTGC
 GAACCAAGACGGAAGAAATCAGTTACTATGTCGATGAAGAG

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa31161.2{*} June 20, 2002 10:41 ..

Table 70: Comparative Sequences relating to SAG 1280

msa31161.2{327dNt_2603}	GgAGGGAAAA	TGAATCAAGA	AGTCTTACTA	CAAATGATGA	GAGCCACTAT
msa31161.2{327d_18RS21}	GnAGGGAAAA	TGAATCAAGA	AGTCTTACTA	CAAATGATGA	GAGCCACTAT
msa31161.2{327dNT_H36B}	GgAGGGAAAA	TGAATCAAGA	AGTCTTACTA	CAAATGATGA	GAGCCACTAT
Consensus	*-*****	*****	*****	*****	*****
	51				100
msa31161.2{327dNt_2603}	TCCTCGTGAT	AGAGCCTTGC	TTGAGGCATT	TTTATATTAC	CAAGCAGAGC
msa31161.2{327d_18RS21}	TCCTCGTGAT	AGAGCCTTGC	TTGAGGCATT	TTTATATTAC	CAAGCAGAGC
msa31161.2{327dNT_H36B}	TCCTCGTGAT	AGAGCCTTGC	TTGAGGCATT	TTTATATTAC	CAAGCAGAGC
Consensus	*****	*****	*****	*****	*****
	101				150
msa31161.2{327dNt_2603}	ATTTTGATGA	GGAGTGGGAT	AGTCTTATTC	ATCAGTTTAT	GACCAATAGG
msa31161.2{327d_18RS21}	ATTTTGATGA	GGAGTGGGAT	AGTCTTATTC	ATCAGTTTAT	GACCAATAGG
msa31161.2{327dNT_H36B}	ATTTTGATGA	GGAGTGGGAT	AGTCTTATTC	ATCAGTTTAT	GACCAATAGG
Consensus	*****	*****	*****	*****	*****
	151				200
msa31161.2{327dNt_2603}	CAAGAAATAA	ATAAGTCTGT	TCAAGTACTT	CACTTTGAGA	CAGATGTTTC
msa31161.2{327d_18RS21}	CAAGAAATAA	ATAAGTCTGT	TCAAGTACTT	CACTTTGAGA	CAGATGTTTC
msa31161.2{327dNT_H36B}	CAAGAAATAA	ATAAGTCTGT	TCAAGTACTT	CACTTTGAGA	CAGATGTTTC
Consensus	*****	*****	*****	*****	*****
	201				250
msa31161.2{327dNt_2603}	AGCTTTTGTC	CAGGCTAGTC	CTTATGATAC	TGCTCATGAT	CTATTGACCT
msa31161.2{327d_18RS21}	AGCTTTTGTC	CAGGCTAGTC	CTTATGATAC	TGCTCATGAT	CTATTGACCT
msa31161.2{327dNT_H36B}	AGCTTTTGTC	CAGGCTAGTC	CTTATGATAC	TGCTCATGAT	CTATTGACCT
Consensus	*****	*****	*****	*****	*****
	251				300
msa31161.2{327dNt_2603}	ATACACAAGT	TTTCGGCCAA	AGTGGTCTTC	AAAACTAGA	TAAACTATCG
msa31161.2{327d_18RS21}	ATACACAAGT	TTTCGGCCAA	AGTGGTCTTC	AAAACTAGA	TAAACTATCG
msa31161.2{327dNT_H36B}	ATACACAAGT	TTTCGGCCAA	AGTGGTCTTC	AAAACTAGA	TAAACTATCG
Consensus	*****	*****	*****	*****	*****
	301				350
msa31161.2{327dNt_2603}	CCGTCCTGAAA	AAAACCTGGT	GATAGAAGTG	GCCTTGTTCA	ATCTGGCCAC
msa31161.2{327d_18RS21}	CCGTCCTGAAA	AAAACCTGGT	GATAGAAGTG	GCCTTGTTCA	ATCTGGCCAC
msa31161.2{327dNT_H36B}	CCGTCCTGAAA	AAAACCTGGT	GATAGAAGTG	GCCTTGTTCA	ATCTGGCCAC
Consensus	*****	*****	*****	*****	*****
	351				400
msa31161.2{327dNt_2603}	TCGTTTTCAA	TTATTGGATT	CCAATGGACA	CTACCAAACC	ATATCGCCGG
msa31161.2{327d_18RS21}	TCGTTTTCAA	TTATTGGATT	CCAATGGACA	CTACCAAACC	ATATCGCCGG
msa31161.2{327dNT_H36B}	TCGTTTTCAA	TTATTGGATT	CCAATGGACA	CTACCAAACC	ATATCGCCGG
Consensus	*****	*****	*****	*****	*****
	401				450
msa31161.2{327dNt_2603}	ATTCACCTCT	ACAAAAGAGT	AGGGGAGCTA	ATTGGGTCAA	TGTGTATCGT
msa31161.2{327d_18RS21}	ATTCACCTCT	ACAAAAGAGT	AGGGGAGCTA	ATTGGGTCAA	TGTGTATCGT
msa31161.2{327dNT_H36B}	ATTCACCTCT	ACAAAAGAGT	AGGGGAGCTA	ATTGGGTCAA	TGTGTATCGT
Consensus	*****	*****	*****	*****	*****
	451				500
msa31161.2{327dNt_2603}	GTGGCTAATA	ATTTAGCGGA	TCGTATTAGT	CGAGATATTG	AACAGTTTCT
msa31161.2{327d_18RS21}	GTGGCTAATA	ATTTAGCGGA	TCGTATTAGT	CGAGATATTG	AACAGTTTCT
msa31161.2{327dNT_H36B}	GTGGCTAATA	ATTTAGCGGA	TCGTATTAGT	CGAGATATTG	AACAGTTTCT
Consensus	*****	*****	*****	*****	*****
	501				550
msa31161.2{327dNt_2603}	CTTAACCTTAC	GAGCCTGAGC	TTGAAACTAG	AGCTGATGAA	ACTGTTCTAG
msa31161.2{327d_18RS21}	CTTAACCTTAC	GAGCCTGAGC	TTGAAACTAG	AGCTGATGAA	ACTGTTCTAG
msa31161.2{327dNT_H36B}	CTTAACCTTAC	GAGCCTGAGC	TTGAAACTAG	AGCTGATGAA	ACTGTTCTAG
Consensus	*****	*****	*****	*****	*****
	551				600
msa31161.2{327dNt_2603}	AAAATGAAGA	AACTGTTGAT	GAGCACAAAA	CAAGTGTTC	TCAAGCAATA
msa31161.2{327d_18RS21}	AAAATGAAGA	AACTGTTGAT	GAGCACAAAA	CAAGTGTTC	TCAAGCAATA
msa31161.2{327dNT_H36B}	AAAATGAAGA	AACTGTTGAT	GAGCACAAAA	CAAGTGTTC	TCAAGCAATA
Consensus	*****	*****	*****	*****	*****
	601				650
msa31161.2{327dNt_2603}	TCITTTTCGAG	AAGAGGGCTC	TCITGGTTATT	GCTAGTTTGG	ATGTAGATT
msa31161.2{327d_18RS21}	TCITTTTCGAG	AAGAGGGCTC	TCITGGTTATT	GCTAGTTTGG	ATGTAGATT
msa31161.2{327dNT_H36B}	TCITTTTCGAG	AAGAGGGCTC	TCITGGTTATT	GCTAGTTTGG	ATGTAGATT
Consensus	*****	*****	*****	*****	*****
	651				700
msa31161.2{327dNt_2603}	GTCTCAACTA	GATGTTCAAA	TAGGAAAAAC	CAGTCATCTG	CCAGCTTATG
msa31161.2{327d_18RS21}	GTCTCAACTA	GATGTTCAAA	TAGGAAAAAC	CAGTCATCTG	CCAGCTTATG
msa31161.2{327dNT_H36B}	GTCTCAACTA	GATGTTCAAA	TAGGAAAAAC	CAGTCATCTG	CCAGCTTATG
Consensus	*****	*****	*****	*****	*****

Table 70: Comparative Sequences relating to SAG 1280

msa31161.2{327dNt_2603}	701				750
	AAGAGTTATC	CTTACGACGT	AAATTTGAGA	TTCTAACATA	TTTTGACCAA
	AAGAGTTATC	CTTACGACGT	AAATTTGAGA	TTCTAACATA	TTTTGACCAA
	msa31161.2{327d_18RS21}	AAGAGTTATC	CTTACGACGT	AAATTTGAGA	TTCTAACATA
msa31161.2{327dNT_H36B}	Consensus	*****	*****	*****	*****
msa31161.2{327dNt_2603}	751				800
	ATTTCGAAATG	AACGTTCCAA	AGTCCCAAGT	TTTAGACGAG	GTGATTTTGA
	ATTTCGAAATG	AACGTTCCAA	AGTCCCAAGT	TTTAGACGAG	GTGATTTTGA
	msa31161.2{327d_18RS21}	ATTTCGAAATG	AACGTTCCAA	AGTCCCAAGT	TTTAGACGAG
msa31161.2{327dNT_H36B}	Consensus	*****	*****	*****	*****
msa31161.2{327dNt_2603}	801				850
	CACAGAGATG	GAAATGACAC	CAGTCTTTGA	TGGCGAGGAA	TTACTTACTT
	CACAGAGATG	GAAATGACAC	CAGTCTTTGA	TGGCGAGGAA	TTACTTACTT
	msa31161.2{327d_18RS21}	CACAGAGATG	GAAATGACAC	CAGTCTTTGA	TGGCGAGGAA
msa31161.2{327dNT_H36B}	Consensus	*****	*****	*****	*****
msa31161.2{327dNt_2603}	851				900
	ATCTCGAAGC	TGATGGCAGT	CCCTATGAGC	TGAAACGAAC	GCTGACTACA
	ATCTCGAAGC	TGATGGCAGT	CCCTATGAGC	TGAAACGAAC	GCTGACTACA
	msa31161.2{327d_18RS21}	ATCTCGAAGC	TGATGGCAGT	CCCTATGAGC	TGAAACGAAC
msa31161.2{327dNT_H36B}	Consensus	*****	*****	*****	*****
msa31161.2{327dNt_2603}	901				950
	GTGGAAGAAA	AGGAATTAGA	AAAAATTGGA	CAAGCCATTA	GGATAGAAAA
	GTGGAAGAAA	AGGAATTAGA	AAAAATTGGA	CAAGCCATTA	GGATAGAAAA
	msa31161.2{327d_18RS21}	GTGGAAGAAA	AGGAATTAGA	AAAAATTGGA	CAAGCCATTA
msa31161.2{327dNT_H36B}	Consensus	*****	*****	*****	*****
msa31161.2{327dNt_2603}	951				1000
	TCAAGAAAAA	TTGACTCAGC	TAAGGATTGa	TTTATCTCAG	TTTGACCCAG
	TCAAGAAAAA	TTGACTCAGC	TAAGGATTGa	TTTATCTCAG	TTTGACCCAG
	msa31161.2{327d_18RS21}	TCAAGAAAAA	TTGACTCAGC	TAAGGATTGr	TTTATCTCAG
msa31161.2{327dNT_H36B}	Consensus	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1001				1050
	ACCGAGTCGG	TATTTTATTG	gATGCAGCAG	GTGCTtTCG	TTTAaAaAAT
	ACCGAGTCGG	TATTTTATTG	gATGCAGCAG	GTGCTtTCG	TTTAaAaAAT
	msa31161.2{327d_18RS21}	ACCGAGTCGG	TATTTTATTG	gATGCAGCAG	GTGCTtTCG
msa31161.2{327dNT_H36B}	Consensus	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1051				1100
	GCAGACCTTG	CTTtACTAGG	TGGTTATCCC	AAAGCCTCGG	TAACCTCACT
	GCAGACCTTG	CTTtACTAGG	TGGTTATCCC	AAAGCCTCGG	TAACCTCACT
	msa31161.2{327d_18RS21}	GCAGACCTTG	CTTtACTAGG	TGGTTATCCC	AAAGCCTCGG
msa31161.2{327dNT_H36B}	Consensus	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1101				1150
	AGCCCTTGCG	ACAGAACTAC	TCCAAATGGG	ACTAAGTCAT	GAAAAGGTTG
	AGCCCTTGCG	ACAGAACTAC	TCCAAATGGG	ACTAAGTCAT	GAAAAGGTTG
	msa31161.2{327d_18RS21}	AGCCCTTGCG	ACAGAACTAC	TCCAAATGGG	ACTAAGTCAT
msa31161.2{327dNT_H36B}	Consensus	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1151				1200
	AAATTTTCTT	TGGTAGCCAG	CTTCCATTG	AAGAGCTGCG	ACAAGTTGCC
	AAATTTTCTT	TGGTAGCCAG	CTTCCATTG	AAGAGCTGCG	ACAAGTTGCC
	msa31161.2{327d_18RS21}	AAATTTTCTT	TGGTAGCCAG	CTTCCATTG	AAGAGCTGCG
msa31161.2{327dNT_H36B}	Consensus	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1201				1250
	TACGCCTTTT	TatACCAAGA	ACTCAGCAGA	GAAGATGCGG	AGCAATTTGA
	TACGCCTTTT	TatACCAAGA	ACTCAGCAGA	GAAGATGCGG	AGCAATTTGA
	msa31161.2{327d_18RS21}	TACGCCTTTT	TatACCAAGA	ACTCAGCAGA	GAAGATGCGG
msa31161.2{327dNT_H36B}	Consensus	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1251				1300
	AAAAGATAAA	GGTAATCAGC	CAGATTTAAC	TCTCAGAGAT	TGGAAAAGCA
	AAAAGATAAA	GGTAATCAGC	CAGATTTAAC	TCTCAGAGAT	TGGAAAAGCA
	msa31161.2{327d_18RS21}	AAAAGATAAA	GGTAATCAGC	CAGATTTAAC	TCTCAGAGAT
msa31161.2{327dNT_H36B}	Consensus	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1301				1350
	AGCTAGAGAA	AGCTGAGGGA	AAAGAAGTAG	TTGATGAAGA	ATTTCGCGAA
	AGCTAGAGAA	AGCTGAGGGA	AAAGAAGTAG	TTGATGAAGA	ATTTCGCGAA
	msa31161.2{327d_18RS21}	AGCTAGAGAA	AGCTGAGGGA	AAAGAAGTAG	TTGATGAAGA
msa31161.2{327dNT_H36B}	Consensus	*****	*****	*****	*****
msa31161.2{327dNt_2603}	1351				1400
	AATCCACTGG	TTCAGAGAGT	ATTGGACACT	TATCCTCTGG	GGTCATTGGT
	AATCCACTGG	TTCAGAGAGT	ATTGGACACT	TATCCTCTGG	GGTCATTGGT
	msa31161.2{327d_18RS21}	AATCCACTGG	TTCAGAGAGT	ATTGGACACT	TATCCTCTGG
msa31161.2{327dNT_H36B}	Consensus	*****	*****	*****	*****

Table 70: Comparative Sequences relating to SAG 1280

msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1401	TTCTTATAAG	GGACAGGACT	TTGAGGTCAT	GTCGGTCAGC	GATGCTCGAT	1450
					TTCTTATAAG	GGACAGGACT	TTGAGGTCAT	GTCGGTCAGC	GATGCTCGAT	
					TTCTTATAAG	GGACAGGACT	TTGAGGTCAT	GTCGGTCAGC	GATGCTCGAT	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1451	TGAACGGTTT	GATTTCGGATT	GAGTTAGTCA	ATGACTTTTC	GGATATCATT	1500
					TGAACGGTTT	GATTTCGGATT	GAGTTAGTCA	ATGACTTTTC	GGATATCATT	
					TGAACGGTTT	GATTTCGGATT	GAGTTAGTCA	ATGACTTTTC	GGATATCATT	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1501	GAACAAAATC	CAGTTCCTTA	TGTGAGGACC	TGGGAAGAAG	TCAGTCAGGC	1550
					GAACAAAATC	CAGTTCCTTA	TGTGAGGACC	TGGGAAGAAG	TCAGTCAGGC	
					GAACAAAATC	CAGTTCCTTA	TGTGAGGACC	TGGGAAGAAG	TCAGTCAGGC	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1551	ACTTCATCAG	CCAAAGGCAG	AACCACAAAC	AGAGTTAGAA	GAAGCGGACC	1600
					ACTTCATCAG	CCAAAGGCAG	AACCACAAAC	AGAGTTAGAA	GAAGCGGACC	
					ACTTCATCAG	CCAAAGGCAG	AACCACAAAC	AGAGTTAGAA	GAAGCGGACC	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1601	AAGAAATAAA	CCTATTCTCA	TTTCTGGAAG	AGGAGCAGT	TCAGAGTATT	1650
					AAGAAATAAA	CCTATTCTCA	TTTCTGGAAG	AGGAGCAGT	TCAGAGTATT	
					AAGAAATAAA	CCTATTCTCA	TTTCTGGAAG	AGGAGCAGT	TCAGAGTATT	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1651	GGACTATTGG	AACCAGATGA	TTCAGAAAAT	GGTCATAACG	ATACTGATCT	1700
					GGACTATTGG	AACCAGATGA	TTCAGAAAAT	GGTCATAACG	ATACTGATCT	
					GGACTATTGG	AACCAGATGA	TTCAGAAAAT	GGTCATAACG	ATACTGATCT	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1701	TGAAGAAACA	GATAATCAAA	TTCTGAAGA	GGAAGTCGTC	GAAACAATTC	1750
					TGAAGAAACA	GATAATCAAA	TTCTGAAGA	GGAAGTCGTC	GAAACAATTC	
					TGAAGAAACA	GATAATCAAA	TTCTGAAGA	GGAAGTCGTC	GAAACAATTC	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1751	CAGAGATTCC	AGTAACGGAC	TTTTATTTTC	CAGAAGATTT	GACGGACTTT	1800
					CAGAGATTCC	AGTAACGGAC	TTTTATTTTC	CAGAAGATTT	GACGGACTTT	
					CAGAGATTCC	AGTAACGGAC	TTTTATTTTC	CAGAAGATTT	GACGGACTTT	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1801	TATCCTAAGA	CTGCTAGAGA	TAAGGTTGAG	ACAAACATTG	TGGCCATTTC	1850
					TATCCTAAGA	CTGCTAGAGA	TAAGGTTGAG	ACAAACATTG	TGGCCATTTC	
					TATCCTAAGA	CTGCTAGAGA	TAAGGTTGAG	ACAAACATTG	TGGCCATTTC	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1851	TTTGGTAAAA	AATCTAGAAG	TAGAGCACCG	CAATGCTTCA	CCAAGTGAAC	1900
					TTTGGTAAAA	AATCTAGAAG	TAGAGCACCG	CAATGCTTCA	CCAAGTGAAC	
					TTTGGTAAAA	AATCTAGAAG	TAGAGCACCG	CAATGCTTCA	CCAAGTGAAC	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1901	AAGAACTCCT	TGCCAAGTAT	GTAGGCTGGG	GTGGACTAGC	CAATGAATTT	1950
					AAGAACTCCT	TGCCAAGTAT	GTAGGCTGGG	GTGGACTAGC	CAATGAATTT	
					AAGAACTCCT	TGCCAAGTAT	GTAGGCTGGG	GTGGACTAGC	CAATGAATTT	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	1951	TTTGATGACT	ATAATCCAAA	ATTTTCTAAG	GAACGAGAAG	AACTGAAGAG	2000
					TTTGATGACT	ATAATCCAAA	ATTTTCTAAG	GAACGAGAAG	AACTGAAGAG	
					TTTGATGACT	ATAATCCAAA	ATTTTCTAAG	GAACGAGAAG	AACTGAAGAG	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	2001	CCTAGTCACA	GATAAAGAGT	ATTCGGATAT	GAAACAGTCC	TCCCTGACAG	2050
					CCTAGTCACA	GATAAAGAGT	ATTCGGATAT	GAAACAGTCC	TCCCTGACAG	
					CCTAGTCACA	GATAAAGAGT	ATTCGGATAT	GAAACAGTCC	TCCCTGACAG	
					*****	*****	*****	*****	*****	
msa31161.2{327dNt_2603}	msa31161.2{327d_18RS21}	msa31161.2{327dNT_H36B}	Consensus	2051	CCTATTACAC	AGACCCATCC	CTGATCCGTC	AGATGTGGGA	TAAGTTGGAA	2100
					CCTATTACAC	AGACCCATCC	CTGATCCGTC	AGATGTGGGA	TAAGTTGGAA	
					CCTATTACAC	AGACCCATCC	CTGATCCGTC	AGATGTGGGA	TAAGTTGGAA	
					*****	*****	*****	*****	*****	

Table 70: Comparative Sequences relating to SAG 1280

Consensus	*****	*****	*****	*****	*****
	2101				2150
msa31161.2{327dNt_2603}	AGAGATGGCT	TTACAGGTGG	CAAAATCCTA	GATCCTTCCA	TGGGAACAGG
msa31161.2{327d_18RS21}	AGAGATGGCT	TTACAGGTGG	CAAAATCCTA	GATCCTTCCA	TGGGAACAGG
msa31161.2{327dNT_H36B}	AGAGATGGCT	TTACAGGTGG	CAAAATCCTA	GATCCTTCCA	TGGGAACAGG
Consensus	*****	*****	*****	*****	*****
	2151				2200
msa31161.2{327dNt_2603}	GAATTTCTTT	GCGGCTATGC	CAAAACACTT	AAGAGAAAAG	AGTGAGTTGT
msa31161.2{327d_18RS21}	GAATTTCTTT	GCGGCTATGC	CAAAACACTT	AAGAGAAAAG	AGTGAGTTGT
msa31161.2{327dNT_H36B}	GAATTTCTTT	GCGGCTATGC	CAAAACACTT	AAGAGAAAAG	AGTGAGTTGT
Consensus	*****	*****	*****	*****	*****
	2201				2250
msa31161.2{327dNt_2603}	ATGGCGTAGA	GTTAGATACT	ATTACAGGAG	CTATTGCCAA	ACACCTTCAT
msa31161.2{327d_18RS21}	ATGGCGTAGA	GTTAGATACT	ATTACAGGAG	CTATTGCCAA	ACACCTTCAT
msa31161.2{327dNT_H36B}	ATGGCGTAGA	GTTAGATACT	ATTACAGGAG	CTATTGCCAA	ACACCTTCAT
Consensus	*****	*****	*****	*****	*****
	2251				2300
msa31161.2{327dNt_2603}	CCCAATAGTC	ATATTGAAAT	TAAGGGATTT	GAGACGGTGG	CTTTTAACGA
msa31161.2{327d_18RS21}	CCCAATAGTC	ATATTGAAAT	TAAGGGATTT	GAGACGGTGG	CTTTTAACGA
msa31161.2{327dNT_H36B}	CCCAATAGTC	ATATTGAAAT	TAAGGGATTT	GAGACGGTGG	CTTTTAACGA
Consensus	*****	*****	*****	*****	*****
	2301				2350
msa31161.2{327dNt_2603}	CAATAGTTTT	GATTTGGTGA	TTTCAAATGT	GCCCTTTGCC	AATATACGAA
msa31161.2{327d_18RS21}	CAATAGTTTT	GATTTGGTGA	TTTCAAATGT	GCCCTTTGCC	AATATACGAA
msa31161.2{327dNT_H36B}	CAATAGTTTT	GATTTGGTGA	TTTCAAATGT	GCCCTTTGCC	AATATACGAA
Consensus	*****	*****	*****	*****	*****
	2351				2400
msa31161.2{327dNt_2603}	TTGCGGATAA	TAGGTACGAT	AGGCCTTACA	TGATTCATGA	CTACTTTGTC
msa31161.2{327d_18RS21}	TTGCGGATAA	TAGGTACGAT	AGGCCTTACA	TGATTCATGA	CTACTTTGTC
msa31161.2{327dNT_H36B}	TTGCGGATAA	TAGGTACGAT	AGGCCTTACA	TGATTCATGA	CTACTTTGTC
Consensus	*****	*****	*****	*****	*****
	2401				2450
msa31161.2{327dNt_2603}	AAAAAGTCAC	TTGATTTGCT	TCATGATGGT	GGACAAGTAG	CGATTATCTC
msa31161.2{327d_18RS21}	AAAAAGTCAC	TTGATTTGCT	TCATGATGGT	GGACAAGTAG	CGATTATCTC
msa31161.2{327dNT_H36B}	AAAAAGTCAC	TTGATTTGCT	TCATGATGGT	GGACAAGTAG	CGATTATCTC
Consensus	*****	*****	*****	*****	*****
	2451				2500
msa31161.2{327dNt_2603}	TTCCACAGGA	ACTATGGATA	AGCGAACAGA	AAACATCTTA	CAAGATATTC
msa31161.2{327d_18RS21}	TTCCACAGGA	ACTATGGATA	AGCGAACAGA	AAACATCTTA	CAAGATATTC
msa31161.2{327dNT_H36B}	TTCCACAGGA	ACTATGGATA	AGCGAACAGA	AAACATCTTA	CAAGATATTC
Consensus	*****	*****	*****	*****	*****
	2501				2550
msa31161.2{327dNt_2603}	GTGAGACAAC	TGAATTTCTT	GGTGGGGTTC	GACTGCCTGA	CTCTGCCTTT
msa31161.2{327d_18RS21}	GTGAGACAAC	TGAATTTCTT	GGTGGGGTTC	GACTGCCTGA	CTCTGCCTTT
msa31161.2{327dNT_H36B}	GTGAGACAAC	TGAATTTCTT	GGTGGGGTTC	GACTGCCTGA	CTCTGCCTTT
Consensus	*****	*****	*****	*****	*****
	2551				2600
msa31161.2{327dNt_2603}	AAGGCCATTG	CAGGAACGAG	TGTCACAACG	GATATGTTAT	TCITCCAGAA
msa31161.2{327d_18RS21}	AAGGCCATTG	CAGGAACGAG	TGTCACAACG	GATATGTTAT	TCITCCAGAA
msa31161.2{327dNT_H36B}	AAGGCCATTG	CAGGAACGAG	TGTCACAACG	GATATGTTAT	TCITCCAGAA
Consensus	*****	*****	*****	*****	*****
	2601				2650
msa31161.2{327dNt_2603}	ACACTTAGAC	AAGGGATATG	TGGCAGACGA	TTTAGCCTTT	TCAGGTTCCA
msa31161.2{327d_18RS21}	ACACTTAGAC	AAGGGATATG	TGGCAGACGA	TTTAGCCTTT	TCAGGTTCCA
msa31161.2{327dNT_H36B}	ACACTTAGAC	AAGGGATATG	TGGCAGACGA	TTTAGCCTTT	TCAGGTTCCA
Consensus	*****	*****	*****	*****	*****
	2651				2700
msa31161.2{327dNt_2603}	TTTCGCTATGA	CAAGGATAGT	CGCATTTGGC	TCAATCCTTA	TTTTGATGGA
msa31161.2{327d_18RS21}	TTTCGCTATGA	CAAGGATAGT	CGCATTTGGC	TCAATCCTTA	TTTTGATGGA
msa31161.2{327dNT_H36B}	TTTCGCTATGA	CAAGGATAGT	CGCATTTGGC	TCAATCCTTA	TTTTGATGGA
Consensus	*****	*****	*****	*****	*****
	2701				2750
msa31161.2{327dNt_2603}	GAATACAATA	GCCAGGTGCT	AGGAACCTAC	GAGGTCAGGA	ATTTTAACGG
msa31161.2{327d_18RS21}	GAATACAATA	GCCAGGTGCT	AGGAACCTAC	GAGGTCAGGA	ATTTTAACGG
msa31161.2{327dNT_H36B}	GAATACAATA	GCCAGGTGCT	AGGAACCTAC	GAGGTCAGGA	ATTTTAACGG
Consensus	*****	*****	*****	*****	*****
	2751				2800
msa31161.2{327dNt_2603}	AGGAACACTT	TCTGTTAAGG	GGACTAGTGA	TGACTTGATT	GCAAGTGTG
msa31161.2{327d_18RS21}	AGGAACACTT	TCTGTTAAGG	GGACTAGTGA	TGACTTGATT	GCAAGTGTG

Table 70: Comparative Sequences relating to SAG 1280

msa31161.2{327dNT_H36B}	AGGAACACTT	TCTGTTAAGG	GGACTAGTGA	TGACTTGATT	GCAAGTGTTG
Consensus	*****	*****	*****	*****	*****
	2801				2850
msa31161.2{327dNt_2603}	AAACAGCTCT	AAATCACGTT	AAGGCCCAA	GAGAGATTGA	TAGAAATGAG
msa31161.2{327d_18RS21}	AAACAGCTCT	AAATCACGTT	AAGGCCCAA	GAGAGATTGA	TAGAAATGAG
msa31161.2{327dNT_H36B}	AAACAGCTCT	AAATCACGTT	AAGGCCCAA	GAGAGATTGA	TAGAAATGAG
Consensus	*****	*****	*****	*****	*****
	2851				2900
msa31161.2{327dNt_2603}	GTCATCATT	ACCCAGATGT	GTTGACCAA	CAAGTCAATG	ATACCTCCAT
msa31161.2{327d_18RS21}	GTCATCATT	ACCCAGATGT	GTTGACCAA	CAAGTCAATG	ATACCTCCAT
msa31161.2{327dNT_H36B}	GTCATCATT	ACCCAGATGT	GTTGACCAA	CAAGTCAATG	ATACCTCCAT
Consensus	*****	*****	*****	*****	*****
	2901				2950
msa31161.2{327dNt_2603}	TCCAGCTGAA	ATGAGGGAAA	ATCTAGGTCA	GTACAGTTT	GGTTATCAGG
msa31161.2{327d_18RS21}	TCCAGCTGAA	ATGAGGGAAA	ATCTAGGTCA	GTACAGTTT	GGTTATCAGG
msa31161.2{327dNT_H36B}	TCCAGCTGAA	ATGAGGGAAA	ATCTAGGTCA	GTACAGTTT	GGTTATCAGG
Consensus	*****	*****	*****	*****	*****
	2951				3000
msa31161.2{327dNt_2603}	GGTCTACAGT	TTACTATCGA	GATAACAAAG	GCATTTCGAGT	CGGAACCAAG
msa31161.2{327d_18RS21}	GGTCTACAGT	TTACTATCGA	GATAACAAAG	GCATTTCGAGT	CGGAACCAAG
msa31161.2{327dNT_H36B}	GGTCTACAGT	TTACTATCGA	GATAACAAAG	GCATTTCGAGT	CGGAACCAAG
Consensus	*****	*****	*****	*****	*****
	3001			3033	
msa31161.2{327dNt_2603}	ACGGAAGAAA	TCAGTTACTA	TGTCGATGAA	GAG	
msa31161.2{327d_18RS21}	ACGGAAGAAA	TCAGTTACTA	TGTCGATGAA	GAG	
msa31161.2{327dNT_H36B}	ACGGAAGAAA	TCAGTTACTA	TGTCGATGAA	GAG	
Consensus	*****	*****	*****	***	

SEQ ID. NO. 7004

STRAIN H36B frame: 1

GGKMNQEVLLQMMRATIPDRALLEAFLLYQAEHFDDEWDSLIHQFMTNRQEIINKSVQVL
HFETDVSAFVQASPYDTAHDLLTYTQVFGQSGLQKLDKLSPEKNLVIEVALFNLATRFQ
LLDSNGHYQTISPDSLQKSRGANLVNVYRVANNLADRI SRDIEQFLTYEPELETRADE
TVLENEETVDEHKTSHVQAI SFREEGSLVIA SLDVDLSQLDVQIGKTSHPAYEELSRLR
KFEILTYFDQIRNERSKVPSFRRGDFDTEMENTPVFDGEELLTYLEADGSPYELKRTLT
VEEKELEKIGQAI RIEENQEKLTQLXIXLSQFDPDRVGILLXAGRXRLKNADLASLGGYP
KASVTQLALATELLQMGSLSEKVEFFFGSLSIEELRQVAYAFHQLSREDAEQFEKDK
GNQPDLTLRDWKSKLEKAEKEVVDEEFAENPLVQVRVLDITYPLGSLVSYKGQDFEVM SVS
DARLNGLRIRIELVNDFSDI IEQNPLVYVRTWEEVSQALHQPKAEPQTELEADQELNLF
FLEELVQSIGLLEPDDSENGHNDTLEETDNQIP EEEVETIPEIPVTDIFYFPEDLTDF
YPKTARDKVETNI VAI RLKVNLEVEHRNASPSEQELLAKYVGWGLANEFFDDYNPKFSK
EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMWDKLERDGTGGKILDPMTGTGNFF
AAMPKHLREKSELYGVELDTITGAI AKHLHPNSHIEIKGFETVAFNDNSFDLVI SNVPFA
NIRIADNRYDRPYMIHDYFVKKSLDLLHDGGQVAI ISSTGTMDKRTENILQDIRETTEFL
GGVRLPDSAFKAIAGTSVTTDMLFFQKHLKGYVADDLAFSGSIRYDKDSRIWLNPFYFDG
EYNSQVLGTYEVRNFGGTL SVKGTSDDLIASVETALNHVKAPREIDRNEVI INPDVLTK
QVNDTSIPAEMRENLGQYSFGYQGSTVYVYRDNGKIRVGTKTEEISYYVDEE

SEQ ID. NO. 7005

STRAIN 18RS21 frame: 1

GGKMNQEVLLQMMRATIPDRALLEAFLLYQAEHFDDEWDSLIHQFMTNRQEIINKSVQVL
HFETDVSAFVQASPYDTAHDLLTYTQVFGQSGLQKLDKLSPEKNLVIEVALFNLATRFQ
LLDSNGHYQTISPDSLQKSRGANLVNVYRVANNLADRI SRDIEQFLTYEPELETRADE
TVLENEETVDEHKTSHVQAI SFREEGSLVIA SLDVDLSQLDVQIGKTSHPAYEELSRLR
KFEILTYFDQIRNERSKVPSFRRGDFDTEMENTPVFDGEELLTYLEADGSPYELKRTLT
VEEKELEKIGQAI RIEENQEKLTQLGIDLSQFDPDRVGILLDAAGFRRLKNADLALLGGYP
KASVTQLALATELLQMGSLSEKVEFFFGSLSIEELRQVAYAFHQLSREDAEQFEKDK
GNQPDLTLRDWKSKLEKAEKEVVDEEFAENPLVQVRVLDITYPLGSLVSYKGQDFEVM SVS
DARLNGLRIRIELVNDFSDI IEQNPLVYVRTWEEVSQALHQPKAEPQTELEADQELNLF
FLEELVQSIGLLEPDDSENGHNDTLEETDNQIP EEEVETIPEIPVTDIFYFPEDLTDF
YPKTARDKVETNI VAI RLKVNLEVEHRNASPSEQELLAKYVGWGLANEFFDDYNPKFSK
EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMWDKLERDGTGGKILDPMTGTGNFF
AAMPKHLREKSELYGVELDTITGAI AKHLHPNSHIEIKGFETVAFNDNSFDLVI SNVPFA
NIRIADNRYDRPYMIHDYFVKKSLDLLHDGGQVAI ISSTGTMDKRTENILQDIRETTEFL
GGVRLPDSAFKAIAGTSVTTDMLFFQKHLKGYVADDLAFSGSIRYDKDSRIWLNPFYFDG
EYNSQVLGTYEVRNFGGTL SVKGTSDDLIASVETALNHVKAPREIDRNEVI INPDVLTK
QVNDTSIPAEMRENLGQYSFGYQGSTVYVYRDNGKIRVGTKTEEISYYVDEE

SEQ ID. NO. 7006

STRAIN 2603 frame: 1

GGKMNQEVLLQMMRATIPDRALLEAFLLYQAEHFDDEWDSLIHQFMTNRQEIINKSVQVL
HFETDVSAFVQASPYDTAHDLLTYTQVFGQSGLQKLDKLSPEKNLVIEVALFNLATRFQ
LLDSNGHYQTISPDSLQKSRGANLVNVYRVANNLADRI SRDIEQFLTYEPELETRADE
TVLENEETVDEHKTSHVQAI SFREEGSLVIA SLDVDLSQLDVQIGKTSHPAYEELSRLR
KFEILTYFDQIRNERSKVPSFRRGDFDTEMENTPVFDGEELLTYLEADGSPYELKRTLT
VEEKELEKIGQAI RIEENQEKLTQLGIDLSQFDPDRVGILLDAAGFRRLKNADLALLGGYP
KASVTQLALATELLQMGSLSEKVEFFFGSLSIEELRQVAYAFHQLSREDAEQFEKDK
GNQPDLTLRDWKSKLEKAEKEVVDEEFAENPLVQVRVLDITYPLGSLVSYKGQDFEVM SVS

Table 70: Comparative Sequences relating to SAG 1280

DARLNGLIRIELVNDFSDIIEQNPLYVVRTWEEVSQALHQPKEPQTELEBDAQELNLFSLFLEEEPVQSIGLLEPDDSENGHNDTDLEETDNQIPPEEEVETIPEIPVTDFFYPEDLTDFYPKTARDKVTENIVAIRLVNLEVEHRNASEQELLAKYVGWGLANEFFDDYNPKFSKEREELKSLVTDKEYSDMKQSSLTAYYTDPSLRIRQMWDLERDGTGGKILDPDSMGTGNNFAAMPKHLREKSELYGVELDTITGAIKHLHPNSHIEIKGFETVAFNDSFDLVI SNVFFANIRIADNRYDRPYMIHDYFVKSLDLLHDGGQVAIISSTGTMDKRTENILQDIRETTEFLGGVRLPDSAFKAIAGTSVTMDMLFFQKHLDKGYVADDLAFSGSIRYDKDSRIWLNPFYDGEYNSQVLGTYEVRNFGGTLVSVKGTSDDLIASVETALNHVKAPREIDRNEVINPDLVTKQVNDTSIPAEEMRENLGQYSPGYQGSTVYVRDNGKIRVGTKEEISYYVDEE

PRETTY of: /biotmp/msa23816.2{*} June 20, 2002 11:04 ..

msa23816.2{327dNT_H36B}	1	50
msa23816.2{327dNT_2603}	gGKMNQEVLL QMMRATIPRD RALLEAFLLY QAEHFDEEWD SLIHQFMTNR	
msa23816.2{327d_18RS21}	gGKMNQEVLL QMMRATIPRD RALLEAFLLY QAEHFDEEWD SLIHQFMTNR	
Consensus	-***** ***** ***** ***** *****	
msa23816.2{327dNT_H36B}	51	100
msa23816.2{327dNT_2603}	QEINKSVQVL HFETDVSAFV QASPYDTAHD LLTYTQVFGQ SGLQKLDKLS	
msa23816.2{327d_18RS21}	QEINKSVQVL HFETDVSAFV QASPYDTAHD LLTYTQVFGQ SGLQKLDKLS	
Consensus	***** ***** ***** ***** *****	
msa23816.2{327dNT_H36B}	101	150
msa23816.2{327dNT_2603}	PSEKNLVIEV ALFNLATRFQ LLDSNGHYQT ISPDSLLQKS RANLVNVYR	
msa23816.2{327d_18RS21}	PSEKNLVIEV ALFNLATRFQ LLDSNGHYQT ISPDSLLQKS RANLVNVYR	
Consensus	***** ***** ***** ***** *****	
msa23816.2{327dNT_H36B}	151	200
msa23816.2{327dNT_2603}	VANNLADRIS RDIEQFLITY EPELETRADE TVLENEETVD EHKTSVHQAI	
msa23816.2{327d_18RS21}	VANNLADRIS RDIEQFLITY EPELETRADE TVLENEETVD EHKTSVHQAI	
Consensus	***** ***** ***** ***** *****	
msa23816.2{327dNT_H36B}	201	250
msa23816.2{327dNT_2603}	SFREGSLVI ASLDVDLSQL DVQIGKTSHL PAYEELSLRR KFEILTYFDQ	
msa23816.2{327d_18RS21}	SFREGSLVI ASLDVDLSQL DVQIGKTSHL PAYEELSLRR KFEILTYFDQ	
Consensus	***** ***** ***** ***** *****	
msa23816.2{327dNT_H36B}	251	300
msa23816.2{327dNT_2603}	IRNERSKVPS FRRGDFDTEM EMTPVFDGEE LLTYLEADGS PYELKRTLIT	
msa23816.2{327d_18RS21}	IRNERSKVPS FRRGDFDTEM EMTPVFDGEE LLTYLEADGS PYELKRTLIT	
Consensus	***** ***** ***** ***** *****	
msa23816.2{327dNT_H36B}	301	350
msa23816.2{327dNT_2603}	VEEKELEKIG QAIRIENQEK LTQLxIxLSQ FDPDRVGILL xAAGRrRLxN	
msa23816.2{327d_18RS21}	VEEKELEKIG QAIRIENQEK LTQLgIdLSQ FDPDRVGILL dAAGRrRLkN	
Consensus	***** ***** *-*** ***** -***-***	
msa23816.2{327dNT_H36B}	351	400
msa23816.2{327dNT_2603}	ADLAsLGGYP KASVTQLALA TELLQMGLSH EKVEFFFGSQ LSIEELRQVA	
msa23816.2{327d_18RS21}	ADLAlLGGYP KASVTQLALA TELLQMGLSH EKVEFFFGSQ LSIEELRQVA	
Consensus	***-***** ***** ***** ***** *****	
msa23816.2{327dNT_H36B}	401	450
msa23816.2{327dNT_2603}	YAFhQELSR EDAAQFEKDK GNQPDLTLD WSKLEKAEG KEVVDEEFAB	
msa23816.2{327d_18RS21}	YAFlyQELSR EDAAQFEKDK GNQPDLTLD WSKLEKAEG KEVVDEEFAB	
Consensus	***-***** ***** ***** ***** *****	
msa23816.2{327dNT_H36B}	451	500
msa23816.2{327dNT_2603}	NPLVQRVLDY YPLGSLVSYK QDQFEVMSVS DARLNGLIRI ELVNDFSDI	
msa23816.2{327d_18RS21}	NPLVQRVLDY YPLGSLVSYK QDQFEVMSVS DARLNGLIRI ELVNDFSDI	
Consensus	***** ***** ***** ***** *****	
msa23816.2{327dNT_H36B}	501	550
msa23816.2{327dNT_2603}	EQNPVLYVRT WEEVSQALHQ PKAEPQTELE EADQELNLFSLFLEEEpVQSI	
msa23816.2{327d_18RS21}	EQNPVLYVRT WEEVSQALHQ PKAEPQTELE EADQELNLFSLFLEEEpVQSI	
Consensus	***** ***** ***** ***** *****	
msa23816.2{327dNT_H36B}	551	600
msa23816.2{327dNT_2603}	GLLEPDDSEN GHNDTDLEET DNQIPPEEEV ETIPEIPVTD FYFPEDLTDF	
msa23816.2{327d_18RS21}	GLLEPDDSEN GHNDTDLEET DNQIPPEEEV ETIPEIPVTD FYFPEDLTDF	
Consensus	***** ***** ***** ***** *****	

Table 70: Comparative Sequences relating to SAG 1280

	601				650
msa23816.2{327dNT_H36B}	YPKTARDKVE	TNIVAIRLVK	NLEVEHRNAS	PSEQELLAKY	VGWGGLANEF
msa23816.2{327dNT_2603}	YPKTARDKVE	TNIVAIRLVK	NLEVEHRNAS	PSEQELLAKY	VGWGGLANEF
msa23816.2{327d_18RS21}	YPKTARDKVE	TNIVAIRLVK	NLEVEHRNAS	PSEQELLAKY	VGWGGLANEF
Consensus	*****	*****	*****	*****	*****
	651				700
msa23816.2{327dNT_H36B}	FDDYNPKFSK	EREELKSLVT	DKEYSDMKQS	SLTAYYTDPS	LIRQMWDKLE
msa23816.2{327dNT_2603}	FDDYNPKFSK	EREELKSLVT	DKEYSDMKQS	SLTAYYTDPS	LIRQMWDKLE
msa23816.2{327d_18RS21}	FDDYNPKFSK	EREELKSLVT	DKEYSDMKQS	SLTAYYTDPS	LIRQMWDKLE
Consensus	*****	*****	*****	*****	*****
	701				750
msa23816.2{327dNT_H36B}	RDGFTGGKIL	DPSMGTGNFF	AAMPKHLREK	SELYGVELDT	ITGAIAKHLH
msa23816.2{327dNT_2603}	RDGFTGGKIL	DPSMGTGNFF	AAMPKHLREK	SELYGVELDT	ITGAIAKHLH
msa23816.2{327d_18RS21}	RDGFTGGKIL	DPSMGTGNFF	AAMPKHLREK	SELYGVELDT	ITGAIAKHLH
Consensus	*****	*****	*****	*****	*****
	751				800
msa23816.2{327dNT_H36B}	PNSHIEIKGF	ETVAFNDNSF	DLVISNVPFA	NIRIADNRYD	RPYMIHDYFV
msa23816.2{327dNT_2603}	PNSHIEIKGF	ETVAFNDNSF	DLVISNVPFA	NIRIADNRYD	RPYMIHDYFV
msa23816.2{327d_18RS21}	PNSHIEIKGF	ETVAFNDNSF	DLVISNVPFA	NIRIADNRYD	RPYMIHDYFV
Consensus	*****	*****	*****	*****	*****
	801				850
msa23816.2{327dNT_H36B}	KKSLDLLHDG	GQVAIISSTG	TMDKRTENIL	QDIRETTEFL	GGVRLPDSAF
msa23816.2{327dNT_2603}	KKSLDLLHDG	GQVAIISSTG	TMDKRTENIL	QDIRETTEFL	GGVRLPDSAF
msa23816.2{327d_18RS21}	KKSLDLLHDG	GQVAIISSTG	TMDKRTENIL	QDIRETTEFL	GGVRLPDSAF
Consensus	*****	*****	*****	*****	*****
	851				900
msa23816.2{327dNT_H36B}	KAIAGTSVTT	DMLFFQKHL	KGYVADDLAF	SGSIRYDKDS	RIWLNPYFDG
msa23816.2{327dNT_2603}	KAIAGTSVTT	DMLFFQKHL	KGYVADDLAF	SGSIRYDKDS	RIWLNPYFDG
msa23816.2{327d_18RS21}	KAIAGTSVTT	DMLFFQKHL	KGYVADDLAF	SGSIRYDKDS	RIWLNPYFDG
Consensus	*****	*****	*****	*****	*****
	901				950
msa23816.2{327dNT_H36B}	EYNSQVLGTY	EVRFNNGGTL	SVKGTSDDLI	ASVETALNHV	KAPREIDRNE
msa23816.2{327dNT_2603}	EYNSQVLGTY	EVRFNNGGTL	SVKGTSDDLI	ASVETALNHV	KAPREIDRNE
msa23816.2{327d_18RS21}	EYNSQVLGTY	EVRFNNGGTL	SVKGTSDDLI	ASVETALNHV	KAPREIDRNE
Consensus	*****	*****	*****	*****	*****
	951				1000
msa23816.2{327dNT_H36B}	VIINPDVLTK	QVNDTSIPAE	MRENLGQYSF	GYQGSTVYYR	DNKGIRVGTK
msa23816.2{327dNT_2603}	VIINPDVLTK	QVNDTSIPAE	MRENLGQYSF	GYQGSTVYYR	DNKGIRVGTK
msa23816.2{327d_18RS21}	VIINPDVLTK	QVNDTSIPAE	MRENLGQYSF	GYQGSTVYYR	DNKGIRVGTK
Consensus	*****	*****	*****	*****	*****
	1001	1011			
msa23816.2{327dNT_H36B}	TEEISYYVDE	E			
msa23816.2{327dNT_2603}	TEEISYYVDE	E			
msa23816.2{327d_18RS21}	TEEISYYVDE	E			
Consensus	*****	*			

Table 71: Comparative Sequences relating to SAG1333

SEQ ID NO. 7101

STRAIN 2603

ATGAAAAAGAAAATTTATTTGAAAAGTAGTGTCTTGGTTTAGTCGCTGGGACTTCTATT
 ATGTTCTCAAGCGTGTTCGCGGACCAAGTCCGGTGTCCAAGTTATAGGCGTCAATGACTTT
 CATGGTGCACCTTGACAATCTGGAACAGCAAAATATGCCTGATGGAAGTTGCTAATGCT
 GGTACTGTCTCAATTAGATGCTTATATGGATGACGCTCAAAAAGATTTCAAACAACT
 AACCCTAATGGTGAAGCATTAGGGTTCAAGCAGGCGATATGGTTGGAGCAAGTCCAGCC
 AACTCTGGGCTTCTTCAAGATGAACCAACTGTCAAAAATTTAATGCAATGAATGTTGAG
 TATGGCACATTGGGTAACCATGAATTTGATGAAGGGTTGGCAGAATATAATCGTATCGTT
 ACTGGTAAAGCCCCGTCTCCAGATTCTAATATTAATAATATTACGAAATCATACCCACAT
 GAAGCTGCAAAACAAAGAAATTTAGTAGTGGCAAAATGTTATGATAAAGTTAAACAAACAAAT
 CCTTACAATTGGAAGCCTTACGCTATTAAAAATATTCCTGTAATAACAAAGTGTGAAC
 GTTGGCTTTATCGGGATTGTCAACAAAGACATCCCAACCTTGTCTTACGTAAAAATTTAT
 GAACAATATGAATTTTAGATGAAGCTGAAACAATCGTTAAATACGCCAAAGAAATTACAA
 GCTAAAAATGTCAAAGCTATTGTAGTTCTCGCACATGTACCTGCAACAAGTAAAAATGAT
 ATTGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCTGAAAAAT
 AGCGTAGATATTGTCTTGTCTGGACACAATCATCAATATACAAATGGTCTTGTGGTAAA
 ACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAGCCTATGTGATGTACGTGGTGTCTTA
 GATACTGATACACAAGATTTCATTGAGACCCCTTCAGCTAAAGTAATTGCAGTTGTCTCT
 GGTAAAAAAGCAGGTAGTCCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTT
 AAACAAGTAAACAGAAAGCAAAAATTTGGTACTGCCAGGTAAAGTGTATGATTACGCGTTCT
 GTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCAGAGGCTCACTAGCAATT
 GCTCGAAAAAGCTGGCCAGATATCGATTTTGGCATGACAATAATGGTGGCATTCTGTCT
 GACTTACTCATCAAAACAGATGGAACAATCACTGGGGAGCTGCACAAGCAGTTCAACCT
 TTTGGTAAATCTTACAAGTCGTGCAAAATTAAGTGGTAGAGATCTTTATAAAGCACTCAAC
 GAACAATACGACCAAAACAAAATTTCTTCTTCAATAGCTGGTCTGCGATACACTTAC
 ACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTGTAAAAGCTTATAAATCA
 AATGGTGAGGAAATCAATCTGATGCAAAATACAAATTAGTTATCAATGACTTTTATTTC
 GGTGGTGGTGTGGCTTTTGGCAAGCTTCAGAAATGCCAAACTTCAGAGGCCATTAAACCC
 GATACAGAGGTATTATGGCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGC
 GTTCCAATAATAAACCTTAAATCTATGTCACTATGAAGATGGTTAATGAACTATTACA
 CAAAATGATGGTACACATAGCATTATTAAAGAACTTTATTAGATCGACAAGGAAATATT
 GTAGCACAAGAGATTGTATCAGACACTTTAAACCAACAAAATCAAAATCTACAAAATC
 AACCTCTAATCTACAAATTCACAAAAACAAATTACACCAATTTACAGCTATTAAACCTATG
 AGAAATTTATGGCAACCATCAAACTCCACTACTGTAAATCAAAACAATTACCAAAAAACA
 AACTCTGAATATGGACAATCAATCCTTATGTCTGTCTTGGTGTGGACTTATAGGAATT
 GCTTTAAATACAAAGAAAAAACATATGAAA

SEQ ID NO. 7102

STRAIN 090

AAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACCTTGAC
 AATACTGGAACAGCAAAATATGCCTGACGGAAGTTACTAATGCTGGCAC
 TGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAAC
 AAATAACCCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATGGTT
 GGAGCAAGTCCAGCTAAGTCAAGGCTTCTCAAGATGAACCAACCGTTAA
 AACATTTAATGCAATGAATGTTGAGTATGGCATTAGGTAACCATGAAT
 TTGATGAAGGTTTGGCAGAATAACAATCGTATCGTTACTGGAAAGGCCCT
 GCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGAAGC
 TGCAAAACAGAAATTTAGTAGTGGCAACGTTATTGATAAAGTTAAACAAAC
 AATCCCTTACAATTTGAAACCTTACGCTATTAAAAATATTCCTGTAAAT
 AACAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAGACATCCC
 AAACCTTGTCTTACGTAAAAATTTATGAACAATATGAATTTTATAGTGAAG
 CTGAAACAATCGTTAATACGCCAAAGAAATTACAAGCTAAAAATGTCAAG
 GCTATTGTAGTCTTGTCTCATGTACCTGCAACCAAGCAAGGATGATATTGC
 TGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCTG
 AAAATAGCTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAAT
 GGTCTTGTGGTAAAACTCGCATTGTACAAGCGCTCTCTCAAGGAAAAGC
 CTATGCTGACGTACGTGGTGTCTTATAGTACTGATACACAAGATTTCATTG
 AAACCCCTTACGCTAAAGTAGTTGAGTGTCTCTGGTAAAAAAGCAGGT
 AGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAACA
 AGTAACAGAAGCTAAATTTGTTACTGCCGAGGTAAGTGGCATGATTACGC
 GTTCTGTTGATCAAGATAATGTTAGTCCAGTAGGCAGCCTCATCAGAG
 GCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGGCCAT
 GACAAATAATGGTGGCATTCTGTCTGACTACTCATCAACCAAGATGGAA
 CAATCACCTGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTTA
 CAAGTCGTGCAAAATTTAGTGGTAGAGATCTTTATAAAGCACTCAACGAACA
 ATACGACCAAAACAAAATTTCTTCTTCAAAATAGCTGGTCTGCGATACA
 CTTACACAGATAATAAAGAGGGCGGAGAAGAAACACCATTTAAAGTTGTA
 AAAGCTTATAAATCAAAATGGTGAAGAAATCAATCCTGATGCAAAATACAA
 ATTAGTTATCAATGACTTTTATTTCGGTGGTGGTGGTGGCTTTGCAAGCT
 TCAGAAATGCCAAACTCTAGGAGCCATTAAATCCCGATACAGAGGTATT
 ATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCGTTCC
 AAATAATAAACCTTAAATCTATGTCACTATGAAGATGGTTAATGAACTA
 TTACACAAAATGATGGTACACATAGCATTATTAAAGAACTTTATTAGAT
 CGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAACCA
 AACAAAATCAAAATCTACAAAATCAACCTGTAACTACAATTCAAAAA
 AACAAATTACCAATTTACAGCTATTAAACCTATGAGAAATTATGGCAAA
 CCATCAAACTCCACTACTGTAAATCAAAACA

SEQ ID NO. 7103

STRAIN A909

GCGTCAATGACTTTTCATGGTGCACCTTGACAATACTGGAACAGCAAAATATG
 CCTGACGGAAGTTACTAATGCTGGCACTGCTGCTCAATTAGATGCTTA

Table 71: Comparative Sequences relating to SAG1333

TATGGATGATGCTCAAAAAGATTTCAAACAACTAACCTTAATGGTGAAA
GCATTAGAGTTCAAGCTGGTGATATGGTTGGAGCAAGTCCAGCTAACTCA
GGGCTTCTTCAAGATGAACCAACCGTTAAAAACATTTAATGCAATGAATGT
TGAGTATGGCACATTAGGTAAACCATGAATTTGATGAAGGTTTGGCAGAAT
ACAATCGTATCGTTACTGGAAGGGCCCTGCTCCaGaTTCTAATATAAAT
AATATTACGAAATCATACCCACAGAGCTGCAAAACAAGAAATTTAGT
GGCAAACGTTATTGATAAAGTTAACAAACAAATCCCTTACAATTGGAAAC
CTTACACTATTAAAAATATTCTGTAAATAACAAAAGTGTGAACGTTGGC
TTTATCGGAATCGTTACCAAGACATCCCAACCTTGTCTTACGTAAAAA
TTATGAACAATATGAATTTTATAGATGAAGCTGAAACAAATCGTTAAATACG
CCAAAGAATTACAAGCTAAAAATGTCAAGGCTATTGTAGTCTTGTCTCAT
GTACCTGCAACAAGCAAGGATGATATTGCTGAAGGTGAAGCAGCAGAAAT
GATGAAAAAAGTCAATCAACTCTTCCCTGAAAAATAGCGTAGATATTGTCT
TTGCTGGACACAATCATCAATATACAAATGGTCTTGTGGTAAAACTCGT
ATTGTACAAGCGCTCTCTCAAGGAAAAGCCTATGCTGATGTCGTGGTGT
CCTAGATACTGATACACAAGATTTTATTGAAACCCCTTCAGCTAAAGTAA
TTGCAAGTTGCTCTGTTAAAAAAGAGGTAGTGGCGATATTCAAGCCATT
GTTGACCAAGCTAATACTATCGTTAAACAGTAACAGAAGCTAAAAATGG
TACTGCCAGGTAAAGTGGCATGATTACGCGTTCTGTTGATCAAGATAATG
TTAGTCCGGTAGGCAGCTCATCACAGAGGCTCAACTAGCAATTGCTCGA
AAAAGCTGGCCAGATATCGATTTTGCCATGACAAATAATGGTGGCATTCG
TGCTGACTTACTCATCAACAGATGGAACAATCACCTGGGGAGCTGCAC
AAGCAGTTCAACCTTTTGGTAATATCTTACAAGTCTGGAATTAAGTGT
AGAGATCTTTATAAGCACTCAACGAACAATACGACCAAAAAACAAATTT
CTTCTTCAAATAGCTGGTCTGCGATACACTTACACAGATAATAAAGAGG
GCGGGGAAGAAACACCATTTAAAGTTGTAAGAGCTTATAAATCAAATGGT
GAGGAAATCAATCCTGATGCAAAATACAAATAGTTATCAATGACTTTT
ATTGGTGGTGGTGGTGGCTTTGCAAGCTTCAGAAATGCCAACTTCTAG
GAGCCATTAAATCCGATACAGAGGTATTTATGGCCTATATCACTGATTTA
GAAAAAGCTGGTAAAAAAGTGAAGCTTCCAAATAATAAACCTAAATCTA
TGTCACTATGAAGATGGTTAATGAACCTATTAACAAATGATGGTACAT
ATAGCATTATTAAGAACTTTATTAGATCGACAAGGAAATATTGTAGCA
CAAGAGATTGTATCAGACACTTTAAACCAACAAATCAAAATCTACAAA
AATCAACCTGTAACTACAATTCAAAAAACAAATTACCAATTTACAG
CTATTAACTTATGAGAAATTTATGGCAACCATCAAACTCCACTACTGTA
AAATCAAAACA

SEQ ID NO. 7104

STRAIN H36B

CCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTATGGTGCATTG
ACAATCTGGAACAGCAAATATGCTGACGGAAGTTACTAATGCTGGC
ACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAGATTTCAA
ACAAACTAACCTTAATGGTGAAGCATTAGAGTTCAAGCTGGTGAATGG
TTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTT
AAAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGA
ATTTGATGAAGTTTGGCAGAATCAATCGTATCGTTACTGGAAAGGCC
CTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACAGAA
GCTGCAAAACAAGAAATTTGATGTCGCAACGTTATTGATAAAGTTAACAA
ACAAATCCCTTACAAATGGAAACCTTACACTATTAAAAATATTCTGTAA
ATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAGACATC
CCAAACCTTGTCTTACGTAAAAATATGAACAATATGAATTTTATAGATGA
AGCTGAAACAATCGTTAAATACGCCAAAGAAATTACAAGCTAAAAATGTCA
AGGCTATTGTAGTCCCTGCTCATGTACCTGCAACAAGCAAGGATGATATT
GCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCC
TGAAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAA
ATGCTCTTGTGGTAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAA
GCCTATGCTGATGTACGTTGGTGTCTTATAGTACTGATACACAAGATTTCAT
TGAAACCCCTTCAGCTAAAGTAAATGTCAGTTGCTTCTGGTAAAAAACAG
GTAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAA
CAAGTAACAGAAAGCTAAAAATGGTACTGCCGAGGTAAGTGGCATGATTAC
CGCTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCTCATCACAG
AGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGGC
ATGACAAATAATGGTGGCATTGCTGCTGACTTACTCATCAACAGATGG
AACAATCACTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCT
TACAAGTCTGCGAAATTAAGTGGTAGAGATCTTTATAAAGCACTCAACGAA
CAATACGACCAAAAAACAAATTTCTTCTTCAAATAGCTGGTCTGCGATA
CACTTACACAGATAATAAGAGGGCGGGGAAGAAACACCAATTTAAAGTTG
TAAAAGCTTATAAATCAAATGGTGAAGAAATCAATCCTGATGCAAAATAC
AAATTAGTTATCAATGACTTTTATTTCGGTGGTGGTGGTGGCTTTGCAAG
CTTCAGAAATGCCAACTTCTAGGAGCCATTAATCCGATACAGAGGTAT
TTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAAGCTT
CCAAATATATAAATCAAAATCTATGTCACTATGAAGATGGTTAATGAAAC
TATTACCAAAATGATGGTACATATAGCATTTATTAAGAACTTTATTTAG
ATCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTAAAC
CAACAAATCAAAATCTACAAAAATCAACCTGTAACTACAATTCACAA
AAAACAATTACACCAATTTACAGCTATTAAACCTATGAGAAATTTATGGCA
AACCATCAAACTCCACTACTGTAATAACAA

SEQ ID NO. 7105

STRAIN 18RS21

GACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTT
ATGGTGCATTGACAATCTGGAACAGCAAATATGCTGACGGAAGGTT
AnTAATGCTGGCACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCA

Table 71: Comparative Sequences relating to SAG1333

AAAAGATTTCAAACAACTAACCCCTAATGGTGAAAGCATTAGAGTTCAAG
 CTGGTGATATGGTTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGAT
 GAACCAACCGTTAAACATTTAATGCAATGAATGTTGAGTATGGCATT
 AGGTAACCATGAATTTGATGAAGTTTGGCAGAATACAACTCGTATCGTTA
 CTGGAAAGGCCCTGCTCCAGATTCTAATATAAATAATATACGAAATCA
 TACCCACACGAAGCTGCAAAACAAGAAATTTAGTAGGCAACGTTATTGA
 TAAAGTTAAACAAACAAATCCCTTACAATTTGGAACCTTACACTATTAAAA
 ATATTCTGTAAATAACAAAGTGTGAACGTTGGCTTTATCGGAATCGTT
 ACCAAAGACATCCCAACCTTGTCTTACGTAAAAATTTATGAACATATGA
 ATTTTTAGATGAAGCTGAACAATCGTTAAATACGCCAAAGAATTACAAG
 CTAAAAATGTCAAGGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGC
 AAGGATGATATTGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAA
 TCAACTCTTCCCTGAAAATAGCGTAGATATTGTCTTGTCTGGACACAATC
 ATCAATATACAAATGGTCTTGTGGTAAACTCGTATTGTACAAGCGCTC
 TCTCAAGGAAAAGCCTATGCTGATGTACGTGGTGTCTTAGATACTGATAC
 ACAAGATTTCATTGAAACCCCTTCAGCTAAAGTAAITGCAAGTTGCTCCTG
 GTAAAAAACAGGTTAGTGGCGATATTCAAGCCATTGTTGACCAAGCTAAT
 ACTATCGTTAAACAAGTAACAGAAGCTAAAATTGGTACTGCCGAGGTAAG
 TGGCATGATTACGCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCA
 GCCTCATCACAGAGGCTCACTAGCAATTTGCTCGAAAAGCTGGCCAGAT
 ATCGATTTTGCCATGACAAATAATGGTGGCATTGCTGCTGACTTACTCAT
 CAAACAGATGGAACAATCACTGGGGAGCTGCACAAGCAGTTCAACCTT
 TTGGTAATATCTTACAAGTCGTGCAAAATTAAGTAGAGATCTTTATAAA
 GCACTCAACGAACAATACGACCAAAAACAAAATTTCTTCTTCAAAATAGC
 TGGTCTGCGATACACTTACACAGATAATAAGAGGGCGGGGAAGAAACAC
 CATTAAAGTTGTAAGCTTATAAATCAAATGGTGAGGAATCAATCCT
 GATGCAAAATACAAATTAGTTATCAATGACTTTTATTTCGGTGGTGGTGA
 TGGCTTTGCAAGCTTCAGAAATGCCAAATCTTAGGAGCCATTATCCCG
 ATACAGAGGTATTTATGGCCATATATCACTGATTAGAAAAAGCTGGTAAA
 AAGGTAGCGTTCCAAATAATAAACCCTAAATCTATGCTCACTATGAAGAT
 GGTTAATGAACTATTACACAAAATGATGGTACATATAGCATTATTAAGA
 AACTTTATTAGATCGACAAGGAATATTGTAGCACAAGAGATTGTATCA
 GACTTTTAAACCAACAAATCAAATCTACAAAATCAACCCGTGAAC
 TACAATTACAAAAACAATTAACCAATTTACAGCTATTAAACCTATGA
 GAAATTATGGCAACCATCAAACTCCACTACTGTAAATCAAA

SEQ ID NO. 7106

STRAIN M732

ACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACTT
 GACAATACCTGGAACAGCAAAATATGCTGACGGAAGTTACTAATGCTGG
 CACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTC
 AACAACTAACCCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATG
 GTTGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGT
 TAAAAATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATG
 AATTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAGGCC
 CCTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGA
 AGCTGCAAAACAAGAAATTTAGTGGCAACGTTATTGATAAAGTTAACA
 AACAAATCCCTTACAATTGGAACCTTACACTATTAAAAATATTCTGTGA
 AATAACAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACAT
 CCCAAACCTTGTCTTACGTAAAAATTAAGAACATATGAATTTTATAGATG
 AAGCTGAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTC
 AAGGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATGATAT
 TGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCC
 CTGAAAAATAGCGTAGATATTGTCTTGTCTGGACACAATCATCAATATACA
 AATGGTCTTGTGTTGGTAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAA
 AGCCTATGCTGATGTACGTGGTGTCTTAGATACTGATACACAAGATTTC
 TTGAAACCCCTTCAGCTAAAGTAATTGCAAGTTGCTCTCTGGTAAAAAACA
 GGTAGTGCCGATATTCAAGCAATTTGTTGACCAAGCTAATACTACTGTTAA
 ACAAGTAACAGAAGCTAAAAATGGTACTGCCGAGGTAAGTGGCATGATTA
 CGCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACA
 GAGGCTCACTAGCAATTGCTCGAAAAGCTGGCCAGATATCGATTTTGTC
 CATGACAAATAATGGTGGCATTCGTGCTGACTTACTCATCAAACAGATG
 GAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATC
 TTACAAGTCGTGCAAAATTAAGTGGTAGAGATCTTTATAAGCACTCAACGA
 ACAATACGACCAAAAACAATAATTTCTTCTTCAATAGCTGGTCTGCGAT
 ACCTTACACAGATAATAAGAGGGCGGGGAAGAAACACCAATTTAAAGTT
 GTAAAGCTTATAAATCAATGGTGAGGAAATCAATCTGATGCAAAATA
 CAAATTAGTTATCAATGACTTTTATTTCGGTGGTGGTATGGCTTTGCAA
 GCTTCAGAAATGCCAACTTCTAGGAGCCATTATCCCGATACAGAGGTA
 TTTATGGCCATATCACTGATTAGAAAAAGCTGGTAAAAAAGTGAGCAT
 TCCAAATAATAAACCTAAAAATCTATGTCACTATGAAGATGGTAAATGAAA
 CTATTACACAAAATGATGGTACATATAGCATTATTAAGAACTTTATTTA
 GATCGACAAGGAATATTGTAGCACAAGAGATTGTATCAGACACTTTAA
 CCAACAAAATCAAATCTACAAAATCAACCCGTGAACCTACAAATTCACA
 AAAAAAATTAACCAATTTACAGCTATTAAACCTATGAGAAATTATGGC
 AACCATCAAACTCCACTACTGTAAATCAAAACA

SEQ ID NO. 7107

STRAIN COH1

ACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACTT
 GACAATACCTGGAACAGCAAAATATGCTGACGGAAGTTACTAATGCTGG
 CACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTC
 AACAACTAACCCCTAATGGTGAAAGCATTAGAGTTCAAGCTGGTGATATG

Table 71: Comparative Sequences relating to SAG1333

GT TGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGT
TAAAAACATTAAATGCAATGAATGTTGAGTATGGCACAATTAGGTAACCATG
AATTTGATGAAGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCC
CCTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGA
AGCTGCAAAACAAGAAATGTAGTGGCAAACGTTATTGATAAAGTTAACA
AACAAATCCCTTACAATTGGAAACCTTACACTATTAAAAATATTCTGTGA
AATAACAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAGACAT
CCCAACCTTGTCTTACGTAAAAATTATGAACAATATGAATTTTATGATG
AAGCTGAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTC
AAGGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATGATAT
TGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCC
CTGAAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACA
AATGGTCTTGTGTTGGTAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAA
AGCCTATGCTGATGTACGTGGTGTCTAGATACTGATACACAAGATTCA
TTGAAACCCCTTCAGCTAAAGTAATTGCAGTTGCTCCTGGTAAAAAACA
GGTAGTGCCGATATTCAAGCCATTGTGACCAAGCTAATACTATCGTTAA
ACAAGTAACAGAAGCTAAAAATGGTACTGCCAGGTAAGTGGCATGATTA
CGCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACA
GAGGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGC
CATGACAAATAATGGTGGCATTCGTGCTGACTTACTCATCAAAACAGATG
GAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATC
TTACAAGTCGTGCAAAATTAAGTGGTAGAGATCTTTATAAAGCACTCAACGA
ACAATACGACCAAAAAACAATAATTTCTTCTCAATAAGCTGGTCTGCGAT
ACACTTACACAGATAATAAGAGGGCGGGGAAGAAACACCATTAAAGTT
GTAAAGCTTATAAATCAAAATGGTGAAGAAATCAATCTGATGCAAAATA
CAAAATTAGTTATCAATGACTTTTATTCTGGTGGTGGTGGTGGCTTTGCAA
GCTTCAGAAATGCCAACTTCTAGGAGCCATTATCCGATACAGAGGTA
TTTATGGCCTATATCACTGATTAGAAAAAGCTGGTAAAAAGTGGAGCAT
TCCAAATAATAAACCCTAAAAATCTATGTCACTATGAAGATGGTTAATGAAA
CTATTACACAAAATGATGGTACATATAGCATTATTAAGAACTTTATTTA
GATCCGACAAGGAAATATGTAGCACAAAGAGATTGTATCAGACACTTTAA
CCAAACAAATCAAAATCTACAAAATCAACCTGTAACTACAATTACAA
AAAAACAATTACCAAAATTTACAGCTATTAAACCCTATGAGAAATTATGGC
AAACCATCAAACTCCACTACTGTAAATCAAA

SEQ ID NO. 7108

STRAIN M781

CAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGCACCTTGA
CAATACTGGAACAGCAAAATATGCCTGACGGAAGTTACTAATGCTGGCA
CTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAA
CAAACTAACCCCTAATGGTGAAGCATTAGAGTTCAAGCTGGTGGATATGGT
TGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTTA
AAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGAA
TTTGTATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAGGCCCC
TGCTCCAGATTCTAATAATAAATAATATTACGAAATCATACCCACACGAAG
CTGCAAAAACAAGAAATGTAGTGGCAAACGTTATTGATAAAGTTAACAAA
CAAAATCCCTTACAATTGGAAACCTTACACTATTAAAAATATTCCTGTAAA
TAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAGACATCC
CAACCTTGTCTTACGTAAAAATTATGAACAATATGAATTTTATGATGAA
GCTGAAACAATCGTTAATAACGCCAAAGAAATACAAGCTAAAAATGTCAA
GGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATGATATTG
CTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCT
GAAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAA
TGGTCTTGTGGTAAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAAG
CCTATGCTGATGTACGTGGTGTCTTAGATACGATACACAAGATTTCATT
GAAACCCCTTCAGCTAAAGTAATTCAGTTGCTCCTGGTAAAAAACAAGG
TAGTGCCGATATTCAAGCCATTGTGACCAAGCTAATACTATCGTTAAAC
AAGTAACAGAAGCTAAATTTGGTACTGCCAGGTAAGTGGCATGATTACG
CGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGA
GGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCA
TGACAAATAATGGTGGCATTCTGTCTGACTTACTCATCAACCCAGATGGA
ACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTT
ACAAGTCGTGCAAAATTACTGGTAGAGATCTTTATAAAGCACTCAACGAAC
AATACGACCAAAAAACAATAATTTCTTCTTCAATAGCTGGTCTCGCATAC
ACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTAAAGTTGT
AAAAGCTTATAAATCAATGGTGAAGAAATCAATCCTGATGCAAAATACA
AATTAGTTATCAATGACTTTTATTCTGGTGGTGGTGGTGGCTTTGCAAGC
TTCAGAAATGCCAACTTCTAGGAGCCATTATCCCGATACAGAGTATT
TATGGCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGGCATTC
CAAAATAAACCCTAAAAATCTATGTCACTATGAAGATGGTTAATGAACT
ATTACACAAAATGATGGTACATATAGCATTATTAAAGAACTTTATTAGAA
TCGACAAGGAAATATGTAGCACAAAGAGATTGTATCAGACACTTTAAACC
AAACAAAATCAAAATCTACAAAATCAACCTGTAACTACAATTACAAA
AAACAATTACACCAATTTACAGCTATTAAACCCTATGAGAAATTATGGCAA
ACCATCAAACTCCACTACTGTAAATCAAA

SEQ ID NO. 7109

STRAIN CJB110

GACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGC
ACTTGACAATACTGGAACAGCAAAATATGCCTGACGGAAGAAAGTTACTAATG
CTGGCACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGAT
TTCAAAACAACTAACCCCTAATGGTGAAGCATTAGAGTTCAAGCTGGTGA
TATGGTTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAA

Table 71: Comparative Sequences relating to SAG1333

CCGTTAAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAAC
 CATGAATTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAG
 GGCCCTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCAC
 ACGAAGCTGCAAAACAGAAATTTAGTGGCAACCGTTATGTATAAAGTT
 AACAAACAAATCCCTTACAATTGGAACCTTACGCTATTAAAAATATTCC
 TGTAAATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAG
 ACATCCCAACCTTGTCTTACGTAAAAATTTATGAACAATATGAATTTTTTA
 GATGAAGCTGAAACAATCGTTAAATACGCCAAAGAAATTACAAGCTAAAAA
 TGTCAAGGCTATTGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATG
 ATATTGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTC
 TTCCTTGAAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATA
 TACAAATGGTCTTGTGGTAAAACTCGCATTGTACAAGCGCTCTCTCAAG
 GAAAAGCCTATGCTGACGTACGTGGTGTCTAGATACTGATACACAAGAT
 TTCATTGAAACCCCTTCAAGTAAAGTAGTTGCAAGTGTCTCTGGTAAAAA
 AACAGGTAGTGGCGATATTCAAGCCATTGTTGACCAAGCTAATATCTATCG
 TTAACAAGCTGAAACAAGCTAAAAATGGTACTGCCGAGGTAAAGTGGCATG
 ATTACGCGTTCTGTTGATCAAGATAATGTTAGTCCAGTAGGCAGCGCTCAT
 CACAGAGCTCAACTAGCAATTGCTCGAAAAAGCTGGCCAGATATCGATT
 TTGCCATGACAAATAATGGTGGCATTCTGTGCTGACTTACTCATCAAAACCA
 GATGGAACAATCACTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAA
 TATCTTACAAGTCTGTCGAAATTAAGTGGTAGAGATCTTTATAAGCACTCA
 ACGAACATACGACCAAAAAACAAATTTCTTCTTCAAATAGCTGGTCTG
 CGATACACTTACACAGATAATAAAGAGGGCGGAGAAGAAACACCATTTAA
 AGTTGTAAAAAGCTTATAAATCAAAATGGTGAAGAAATCAATCTGTGCA
 AATACAAATTAGTTATCAATGACTTTTTATTCTGGTGGTGGTATGGCTTT
 GCAAGCTTCAGAAATGCAAACTTCTAGGAGCCATTAAATCCGATACAGA
 GGTATTTATGGCTTATATCACTGATTTAGAAAAAGCTGGTAAAAAGTGA
 GCGTTCCAAATAATAAACCTAAAAATCTATGTCACTATGAAGATGGTTAAT
 GAACTATTACACAAATGATGGTACACATAGCATTATTAAGAACTTTA
 TTTAGATCGACAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTT
 TAAACCAAAACAAATCAAAATCTACAAATCAACCTGTAACTACAAAT
 CACAAAAACAATTACACCAATTTACAGCTATTAACCTATGAGAAATTA
 TGGCAACCATCAAACTCCACTACTGTAAATCA

SEQ ID NO. 7110

STRAIN 1169NT

CAAGTCCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACCTTGA
 CAATACTGGAACAGCAAAATATGCCCTGATGGAAGAGTTGCTAATGCTGGTA
 CTGCTGCTCAATTAGATGCTTATATGGATGACGCTCAAAAAGATTTCAAA
 CAAACTAACCCCTAATGGTGAAGCATTAGGGTTCAAGCAGGCGATATGGT
 TGGAGCAAGTCCAGCCAACTCTGGCTTCTTCAAGATGAACCAACTGTCA
 AAAATTTTAAATGCAATGAATGTTGAGTATGGCACATTGGGTAAACATGAA
 TTTGATGAAGGGTTGGCAGAAATATAATCGTATCGTTACTGGTAAAGCCCC
 TGCTCCAGATTCTAATATTAATAATTATACGAAATCATACCCACATGAAG
 CTGCAAAACAAGAAATTTAGTGGCAAAATGTTATGATAAGTTTAAACAA
 CAAATTCCTTACAATTGGAAGCCTTACGCTATTAAAAATATTCCTGTAA
 TAACAAAGTGTGAACGTTGGCTTTATCGGGATTGTCACCAAGACATCC
 CAAACCTTGTCTTACGTAAAAATTTATGAACAATATGAATTTTATGATGAA
 GCTGAAACAATCGTTAAATACGCCAAAGAAATTACAAGCTAAAAATGTCAA
 AGCTATTGTAGTCTCGCACATGTACCTGCAACAAGTAAAAATGATATTG
 CTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCT
 GAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAA
 TGGTCTTGTGGTAAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAAG
 CCTATGCTGATGTACGTGGTGTCTTAGATACTGATACACAAGATTTCATT
 GAGACCCCTTCAAGTAAAGTAATTGCAGTTGCTCTGGTAAAAAACAGG
 TAGTGGCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAAC
 AAGTAACAGAAGCTAAATTTGGTACTGCCGAGGTAAGTGTATGATTACG
 CGTTCTGTTGATCAAGATAATGTTAGTCCGCTAGGCAGCCTCATCACAGA
 GGTCAACTAGCAATTTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCA
 TGACAAATAATGGTGGCATTCTGTGCTGACTTACTCATCAAACAGATGGA
 ACAATCACCTGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTT
 ACAAGTCTGCGAAATTAAGTGGTAGAGATCTTTATAAGCACTCAACGAAC
 AATACGACCAAAAAACAAATTTCTTCTTCAAATAGCTGGTCTGCGATAC
 ACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTGT
 AAAAGCTTATAAATCAAAATGGTGAAGGAAATCAATCCTGATGCAAAATACA
 AATTAGTTATCAATGACTTTTATTCTGGTGGTGGTATGGCTTTGCAAGC
 TTCAGAAATGCCAACTCTAGGAGCCATTAAACCCGATACAGAGGTATT
 TATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAGTGAAGCGTTC
 CAAATAATAAACCTAAATCTATGTCACTATGAAGATGGTTAATGAACT
 ATTACACAAATGATGGTACACATAGCATTATTAAGAACTTTATTTAGA
 TCGACAAGGAAATATTGTAGCACAAGAGATTGTATCAGACACTTTAAAC
 AAACAAATCAAAATCTACAAATCAACCTGTAACTACAAATCACAA
 AAACAAATTACCAATTTACAGCTATTAACCTATGAGAAATTTAGCAA
 ACCATCAAACTCCACTACTGTAAATCAAA

SEQ ID NO. 7111

STRAIN JM9130013

CGGTGTCAGATTATAGGCGTCAATGACTTTTCATGGTGCACCTTGACAATA
 CTGGAACAGCAAAATATGCCCTGACGGAAGGTTACTAATGCTGGCACTGCT
 GCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAACAAAC
 TAACCTAATGGTGAAGCATTAGAGTTCAAGCTGGTATGATGGTTGGAG
 CAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTTAAACCA
 TTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAAACATGAATTTGA

Table 71: Comparative Sequences relating to SAG1333

TGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCCCTGCTC
 CAGATTcTAATATAAATAATATTACGAAATCATACCCACACGAAGCTGCA
 AAACAAGAAATTTAGTGGCAACGTTATTTGATAAAGTTAAACAAACAAAT
 CCCTTACAATTTGGAACCTTACACTATTAATAATATTCTGTAAATAACA
 AAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAGACATCCCAAAC
 CTGTCTTACGTAAAAATTATGAACAATATGAATTTTGTAGATGAAGCTGA
 AACAAATCGTTAAATACGCCAAAGAATTACAGCTAAAAATGTCAAGGCTA
 TTGTAGTCTTGTCTCATGTACCTGCAACAGCAAGGATGATATTGCTGAA
 GGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCTGAAAA
 TAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAATGGTC
 TTGTTGGTAAAACTCGTATTGTACAGCGCTCTCTCAAGGAAAAGCCTAT
 GCTGATGTACGTGGTGTCTAGATACCTGATACACAAGATTTTATTGAAAC
 CCCTTCAGCTAAAGTAATTGCAAGTTGCTCCTGGTAAAAAACAGGTAGTG
 CCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAACAAGTA
 ACAGAAGCTAAAAATTTGGTACTGCCGAGGTAAAGTGGCATGATTACGCGTTC
 TGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGAGGCTC
 AACTAGCAATTTGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCATGACA
 AATAATGGTGGCATTCTGTCTGACTTACTCATCAAACAGATGGAACAAT
 CACCTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCTTACAAG
 TCGTCAAAATTTAGTGTAGATCTTTATAAAGCACTCAACGAACAATAC
 GACCAAAAAACAAATTTCTTCTTCAAAATAGCTGGTCTGCGATACACTTA
 CACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTGTAAAG
 CTTATAAATCAAAATGGTGGAGAAATCAATCCTGATGCAAAATACAAATTA
 GTTATCAATGACTTTTATTCGGTGGTGGTGGTGGCTTTGCAAGCTTCAG
 AAATGCCAACTCTTAGGAGCCATTAATCCCGATACAGAGGTATTATGG
 CCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCGTTCCAAT
 AATAAACCTAAAACTATGTCACTATGAAGATGGTTAATGAACTATTAC
 ACAAAATGATGGTACATATAGCATTATTGAGAACTTTATTTAGATCGAC
 AAGGAAATATTGTAGCAACAAGAGATTGTATCAGACACTTTAAACCAACA
 AAATCAAAATCTACAAAATCAACCTGTAACTACAATTACAAAAAACA
 ATTACCAATTTACAGCTATTAAACCTATGAGAAATTTATGGCAACCAT
 CAACTCCACTACTGTAAATCAAAA

PRETTY of: /biotmp/msa237456.2{*} May 14, 2003 03:20 ..

	1				50
msa237456.2{328_1169NT}	-----	-----	-----	-----	-----
msa237456.2{328_2603}	atgaaaaaga	aaattattht	gaaaagtagt	gttcttggtt	tagtcgctgg
msa237456.2{328_18RS21}	-----	-----	-----	-----	-----
msa237456.2{328_H36B}	-----	-----	-----	-----	-----
msa237456.2{328_COH1}	-----	-----	-----	-----	-----
msa237456.2{328_M732}	-----	-----	-----	-----	-----
msa237456.2{328_M781}	-----	-----	-----	-----	-----
msa237456.2{328_JM9130013}	-----	-----	-----	-----	-----
msa237456.2{328_A909}	-----	-----	-----	-----	-----
msa237456.2{328_090}	-----	-----	-----	-----	-----
msa237456.2{328_CJB110}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa237456.2{328_1169NT}	-----	-----	-----	-----	-----
msa237456.2{328_2603}	gacttctatt	atgttctcaa	gcgtgttcgc	gGACcaagtc	ggtgtccaag
msa237456.2{328_18RS21}	-----	-----	-----	-----	-----
msa237456.2{328_H36B}	-----	-----	-----	-----	-----
msa237456.2{328_COH1}	-----	-----	-----	-----	-----
msa237456.2{328_M732}	-----	-----	-----	-----	-----
msa237456.2{328_M781}	-----	-----	-----	-----	-----
msa237456.2{328_JM9130013}	-----	-----	-----	-----	-----
msa237456.2{328_A909}	-----	-----	-----	-----	-----
msa237456.2{328_090}	-----	-----	-----	-----	-----
msa237456.2{328_CJB110}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	101				150
msa237456.2{328_1169NT}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_2603}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_18RS21}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_H36B}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_COH1}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_M732}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_M781}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_JM9130013}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_A909}	-----GCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_090}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
msa237456.2{328_CJB110}	ttatagGCGT	CAATGACTTT	CATGGTGCAC	TTGACAATAC	TGGAACAGCA
Consensus	-----****	*****	*****	*****	*****
	151				200
msa237456.2{328_1169NT}	AATATGCCTG	AtGGAAAAAGT	TgcTAATGCT	GGtACTGCTG	CTCAATTAGA
msa237456.2{328_2603}	AATATGCCTG	AtGGAAAAAGT	TgcTAATGCT	GGtACTGCTG	CTCAATTAGA
msa237456.2{328_18RS21}	AATATGCCTG	AcGGAAAAAGT	TanTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_H36B}	AATATGCCTG	AcGGAAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_COH1}	AATATGCCTG	AcGGAAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_M732}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_M781}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_JM9130013}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_A909}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_CJB110}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
Consensus	*****	*-*****	*-*****	*-*****	*****
msa237456.2{328_1169NT}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_2603}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_18RS21}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_H36B}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_COH1}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_M732}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_M781}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_JM9130013}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_A909}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_090}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
msa237456.2{328_CJB110}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCCTAATG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_2603}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_18RS21}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_H36B}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_COH1}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_M732}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_M781}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_JM9130013}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_A909}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_090}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_CJB110}	GTGAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_2603}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_18RS21}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_H36B}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_COH1}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_M732}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_M781}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_JM9130013}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_A909}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_090}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
msa237456.2{328_CJB110}	AACCTcGGGC	TTCTTCAAGA	TGAACCAAcT	GtCAAAAaT	TTAATGCAAT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
msa237456.2{328_2603}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
msa237456.2{328_18RS21}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
msa237456.2{328_H36B}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
msa237456.2{328_COH1}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
msa237456.2{328_M732}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
msa237456.2{328_M781}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
msa237456.2{328_JM9130013}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
msa237456.2{328_A909}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
msa237456.2{328_090}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
msa237456.2{328_CJB110}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGgTTGG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	CAGAATAcAA	TCGTATCGTT	ACTGGtAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_2603}	CAGAATAcAA	TCGTATCGTT	ACTGGtAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_18RS21}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_H36B}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_COH1}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_M732}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_M781}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_JM9130013}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_A909}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_090}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_CJB110}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAg	CCCCTGCTCC	AGATTCTAAT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	ATtAATAATA	TTACGAAATC	ATACCCACat	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_2603}	ATtAATAATA	TTACGAAATC	ATACCCACat	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_18RS21}	ATaAATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_H36B}	ATaAATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_COH1}	ATaATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_M732}	ATaATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_M781}	ATaATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_JM9130013}	ATaATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_A909}	ATaATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_090}	ATaATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_CJB110}	ATaATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	501	TGTAAGTTAA	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_2603}	TGTAAGTTAA	ATAAAGTTAA	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_18RS21}	TGTAAGTTAA	ATAAAGTTAA	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_H36B}	TGTAAGTTAA	ATAAAGTTAA	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_COH1}	TGTAAGTTAA	ATAAAGTTAA	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_M732}	TGTAAGTTAA	ATAAAGTTAA	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_M781}	TGTAAGTTAA	ATAAAGTTAA	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_JM9130013}	TGTAAGTTAA	ATAAAGTTAA	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_A909}	TGTAAGTTAA	ATAAAGTTAA	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_090}	TGTAAGTTAA	ATAAAGTTAA	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_CJB110}	TGTAAGTTAA	ATAAAGTTAA	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	551	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA
msa237456.2{328_2603}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_18RS21}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_H36B}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_COH1}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_M732}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_M781}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_JM9130013}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_A909}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_090}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_CJB110}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	601	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC
msa237456.2{328_2603}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_18RS21}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_H36B}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_COH1}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_M732}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_M781}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_JM9130013}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_A909}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_090}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_CJB110}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	651	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA
msa237456.2{328_2603}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_18RS21}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_H36B}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_COH1}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_M732}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_M781}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_JM9130013}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_A909}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_090}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_CJB110}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	701	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT
msa237456.2{328_2603}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTc
msa237456.2{328_18RS21}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_H36B}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_COH1}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_M732}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_M781}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_JM9130013}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_A909}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_090}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_CJB110}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	751	GCaCATGTAC	CTGCAACAAG	tAAaaATGAT	ATTGCTGAAG
msa237456.2{328_2603}	GCaCATGTAC	CTGCAACAAG	tAAaaATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_18RS21}	GcCATGTAC	CTGCAACAAG	cAagATGAT	ATTGCTGAAG	GTGAAGCAGC

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_H36B}	GctCATGTAC	CTGCAACAAG	caAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_COH1}	GctCATGTAC	CTGCAACAAG	caAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_M732}	GctCATGTAC	CTGCAACAAG	caAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_M781}	GctCATGTAC	CTGCAACAAG	caAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_JM9130013}	GctCATGTAC	CTGCAACAAG	caAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_A909}	GctCATGTAC	CTGCAACAAG	caAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_O90}	GctCATGTAC	CTGCAACAAG	caAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_CJB110}	GctCATGTAC	CTGCAACAAG	caAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
Consensus	***-*****	*****-***	*****-***	*****-***	*****-***
msa237456.2{328_1169NT}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_2603}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_18RS21}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_H36B}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_COH1}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_M732}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_M781}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_JM9130013}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_A909}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_O90}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_CJB110}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
msa237456.2{328_1169NT}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_2603}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_18RS21}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_H36B}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_COH1}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_M732}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_M781}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_JM9130013}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_A909}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_O90}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_CJB110}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
msa237456.2{328_1169NT}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_2603}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_18RS21}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_H36B}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_COH1}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_M732}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_M781}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_JM9130013}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_A909}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_O90}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_CJB110}	ACTCGcATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
msa237456.2{328_1169NT}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_2603}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_18RS21}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_H36B}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_COH1}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_M732}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_M781}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_JM9130013}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_A909}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_O90}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_CJB110}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
msa237456.2{328_1169NT}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_2603}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_18RS21}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_H36B}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_COH1}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_M732}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_M781}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_JM9130013}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_A909}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_O90}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_CJB110}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
msa237456.2{328_1169NT}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_2603}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_18RS21}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_H36B}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_COH1}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_M732}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_M781}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_JM9130013}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_A909}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_090}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_CJB110}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	AATTGGTACT	GCCGAGGTAA	GTGtCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_2603}	AATTGGTACT	GCCGAGGTAA	GTGtCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_18RS21}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_H36B}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_COH1}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_M732}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_M781}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_JM9130013}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_A909}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_090}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_CJB110}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
Consensus	*****	*****	***_*****	*****	*****
msa237456.2{328_1169NT}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_2603}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_18RS21}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_H36B}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_COH1}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_M732}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_M781}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_JM9130013}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_A909}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_090}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_CJB110}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
Consensus	*****	***_*****	*****	*****	*****
msa237456.2{328_1169NT}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_2603}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_18RS21}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_H36B}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_COH1}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_M732}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_M781}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_JM9130013}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_A909}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_090}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_CJB110}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTIT	GCCATGACAA	ATAATGGTGG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_2603}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_18RS21}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_H36B}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_COH1}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_M732}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_M781}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_JM9130013}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_A909}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_090}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_CJB110}	CATTCTGTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_2603}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_18RS21}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_H36B}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_COH1}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_M732}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_M781}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_JM9130013}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_A909}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_090}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_CJB110}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	ACTGGTAGAG	ATCTTTTATA	AGCACTCAAC	GAACAATACG	ACCAAAAACA
	1351				1400

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_2603}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_18RS21}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_H36B}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_COH1}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_M732}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_M781}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_JM9130013}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_A909}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_090}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_CJB110}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_2603}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_18RS21}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_H36B}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_COH1}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_M732}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_M781}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_JM9130013}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_A909}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_090}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_CJB110}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	AAGAGGGCGG	GGAAGAAACA	CCATTAAAG	TGTAAAAGC	TTATAAATCA
msa237456.2{328_2603}	AAGAGGGCGG	GGAAGAAACA	CCATTAAAG	TGTAAAAGC	TTATAAATCA
msa237456.2{328_18RS21}	AAGAGGGCGG	GGAAGAAACA	CCATTAAAG	TGTAAAAGC	TTATAAATCA
msa237456.2{328_H36B}	AAGAGGGCGG	GGAAGAAACA	CCATTAAAG	TGTAAAAGC	TTATAAATCA
msa237456.2{328_COH1}	AAGAGGGCGG	GGAAGAAACA	CCATTAAAG	TGTAAAAGC	TTATAAATCA
msa237456.2{328_M732}	AAGAGGGCGG	GGAAGAAACA	CCATTAAAG	TGTAAAAGC	TTATAAATCA
msa237456.2{328_M781}	AAGAGGGCGG	GGAAGAAACA	CCATTAAAG	TGTAAAAGC	TTATAAATCA
msa237456.2{328_JM9130013}	AAGAGGGCGG	GGAAGAAACA	CCATTAAAG	TGTAAAAGC	TTATAAATCA
msa237456.2{328_A909}	AAGAGGGCGG	GGAAGAAACA	CCATTAAAG	TGTAAAAGC	TTATAAATCA
msa237456.2{328_090}	AAGAGGGCGG	GGAAGAAACA	CCATTAAAG	TGTAAAAGC	TTATAAATCA
msa237456.2{328_CJB110}	AAGAGGGCGG	GGAAGAAACA	CCATTAAAG	TGTAAAAGC	TTATAAATCA
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_2603}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_18RS21}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_H36B}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_COH1}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_M732}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_M781}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_JM9130013}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_A909}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_090}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_CJB110}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_2603}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_18RS21}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_H36B}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_COH1}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_M732}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_M781}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_JM9130013}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_A909}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_090}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_CJB110}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_2603}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_18RS21}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_H36B}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_COH1}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_M732}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_M781}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_JM9130013}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_A909}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_090}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_CJB110}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_2603}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_18RS21}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_H36B}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_COH1}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_M732}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_M781}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_JM9130013}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_A909}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_090}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_CJB110}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
Consensus	*****	*****	*****	*****	*****

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_1169NT}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_2603}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_18RS21}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_H36B}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_COH1}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	aTTCCAAATA	ATAAACCTAA
msa237456.2{328_M732}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	aTTCCAAATA	ATAAACCTAA
msa237456.2{328_M781}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	aTTCCAAATA	ATAAACCTAA
msa237456.2{328_JM9130013}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_A909}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_090}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_CJB110}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
Consensus	*****	*****	*****	-*****	*****
msa237456.2{328_1169NT}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_2603}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_18RS21}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_H36B}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_COH1}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_M732}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_M781}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_JM9130013}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_A909}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_090}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
msa237456.2{328_CJB110}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACATTATCA	CAAAATGATG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_2603}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_18RS21}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_H36B}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_COH1}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_M732}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_M781}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_JM9130013}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_A909}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_090}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_CJB110}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_2603}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_18RS21}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_H36B}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_COH1}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_M732}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_M781}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_JM9130013}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_A909}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_090}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_CJB110}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	TACAAAAATC	AACCCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_2603}	TACAAAAATC	AACCCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_18RS21}	TACAAAAATC	AACCCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_H36B}	TACAAAAATC	AACCCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_COH1}	TACAAAAATC	AACCCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_M732}	TACAAAAATC	AACCCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_M781}	TACAAAAATC	AACCCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_JM9130013}	TACAAAAATC	AACCCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_A909}	TACAAAAATC	AACCCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_090}	TACAAAAATC	AACCCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_CJB110}	TACAAAAATC	AACCCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	TTACAGCTAT	TAACCCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_2603}	TTACAGCTAT	TAACCCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_18RS21}	TTACAGCTAT	TAACCCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_H36B}	TTACAGCTAT	TAACCCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_COH1}	TTACAGCTAT	TAACCCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_M732}	TTACAGCTAT	TAACCCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_M781}	TTACAGCTAT	TAACCCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_JM9130013}	TTACAGCTAT	TAACCCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_A909}	TTACAGCTAT	TAACCCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_090}	TTACAGCTAT	TAACCCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_CJB110}	TTACAGCTAT	TAACCCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
Consensus	*****	*****	*****	*****	*****

Table 71: Comparative Sequences relating to SAG1333

	1951			2000
msa237456.2{328_1169NT}	ACTGTAAAT CAaa-----	-----	-----	-----
msa237456.2{328_2603}	ACTGTAAAT CAaaACAAtt	accaaaaaaca	aactctgaat	atggacaatc
msa237456.2{328_18RS21}	ACTGTAAAT CAaaA-----	-----	-----	-----
msa237456.2{328_H36B}	ACTGTAAAT CAaa-----	-----	-----	-----
msa237456.2{328_COH1}	ACTGTAAAT CAaa-----	-----	-----	-----
msa237456.2{328_M732}	ACTGTAAAT CAaaACAA--	-----	-----	-----
msa237456.2{328_M781}	ACTGTAAAT CAaa-----	-----	-----	-----
msa237456.2{328_JM9130013}	ACTGTAAAT CAaaA-----	-----	-----	-----
msa237456.2{328_A909}	ACTGTAAAT CAaaACAA--	-----	-----	-----
msa237456.2{328_090}	ACTGTAAAT CAaaACAA--	-----	-----	-----
msa237456.2{328_CJB110}	ACTGTAAAT CA-----	-----	-----	-----
Consensus	***** **_*****	*****	*****	*****
	2001			2050
msa237456.2{328_1169NT}	-----	-----	-----	-----
msa237456.2{328_2603}	attccttatg	tctgtctttg	gtgttggaact	tataggaatt
msa237456.2{328_18RS21}	-----	-----	-----	-----
msa237456.2{328_H36B}	-----	-----	-----	-----
msa237456.2{328_COH1}	-----	-----	-----	-----
msa237456.2{328_M732}	-----	-----	-----	-----
msa237456.2{328_M781}	-----	-----	-----	-----
msa237456.2{328_JM9130013}	-----	-----	-----	-----
msa237456.2{328_A909}	-----	-----	-----	-----
msa237456.2{328_090}	-----	-----	-----	-----
msa237456.2{328_CJB110}	-----	-----	-----	-----
Consensus	*****	*****	*****	*****
	2051			2070
msa237456.2{328_1169NT}	-----	-----	-----	-----
msa237456.2{328_2603}	caaagaaaaa	acatatgaaa	-----	-----
msa237456.2{328_18RS21}	-----	-----	-----	-----
msa237456.2{328_H36B}	-----	-----	-----	-----
msa237456.2{328_COH1}	-----	-----	-----	-----
msa237456.2{328_M732}	-----	-----	-----	-----
msa237456.2{328_M781}	-----	-----	-----	-----
msa237456.2{328_JM9130013}	-----	-----	-----	-----
msa237456.2{328_A909}	-----	-----	-----	-----
msa237456.2{328_090}	-----	-----	-----	-----
msa237456.2{328_CJB110}	-----	-----	-----	-----
Consensus	*****	*****	-----	-----

SEQ ID NO. 7112

STRAIN 2603 frame: 1

MKKKIILKSSVLGLVAGTSIMFSSVFADQVGQVIGVNDPHGALDNTGTANMPDGKVVANA
GTAAQLDAYMDDAQKDFKQTNPNGESIRVQAGDMVGASPANSGLLQDEPTVKNFNAMNVE
YGTLGNEHFEDEGLAEYNIIVTGKAPAPDSNINNITKSPHEAAKQEIIVVANVIDKVNKQI
PYNWKPYAIKNI PVNNKSVNVGFIGIVTKDIPNLVLRKNYEQYEFLEDEAETIVKYAKELQ
AKNVKAIIVLAHVAPATSKDDIAEGEAAEMMKVNLFPENSVDIVFAGHNHQYTNGLVGK
TRIVQALSQGGKAYADVRGVLDTDTQDFIETPSAKVIAVAPGKKTGSADIQAIIVDQANTIV
KQVTEAKIGTAEVSGMITRSVDQDNVSPVGSGLITEAQLAIARKSWPIDFAMTNNGGIRAD
LLIKPDGTITWGAAQAVQPFNGILQVVEITGRDLYKALNEQYDQKQNFLLQIAGLRYTY
TDNKEGGEETPFKVVKAYKSNGBEINPDACYKLVINDFLFGGGDGFASFRNAKLLGAINP
DTEVFMAIITDLEKAGKKVSVPNKPKIYVTMKNVNETITQNDGTHSIIKKLYLDRQGN
VAQEIVSDTLNQTQKSKSTKINPVTTIHKKQLHQFTAINPMRNYGKPSNSTTVKSKQLPKT
NSEYQGSFLMSVFGVGLIGIALNTKKKHKM

SEQ ID NO. 7113

STRAIN 090 frame: 3

VGVQVIGVNDPHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRV
QAGDMVGASPANSGLLQDEPTVKTNFAMNVEYGTLGNEHFEDEGLAEYNIIVTGKAPAPDS
NINNITKSPHEAAKQEIIVVANVIDKVNKQIPYNWKPYAIKNI PVNNKSVNVGFIGIVTK
DIPNLVLRKNYEQYEFLEDEAETIVKYAKELQAKNVKAIIVLAHVAPATSKDDIAEGEAAEM
MKVNLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGGKAYADVRGVLDTDTQDFIET
PSAKVIAVAPGKKTGSADIQAIIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSPV
GSLITEAQLAIARKSWPIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFNGILQVVE
ITGRDLYKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGBEINPD
KYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVPNKPKIY
VTMKNVNETITQNDGTHSIIKKLYLDRQGNIVAQEIVSDTLNQTQKSKSTKINPVTTIHKK
QLHQFTAINPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7114

STRAIN A909 frame: 3

VNDPHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRVQAGDMVG
ASPANSGLLQDEPTVKTNFAMNVEYGTLGNEHFEDEGLAEYNIIVTGKAPAPDSNINNITK
SPHEAAKQEIIVVANVIDKVNKQIPYNWKPYAIKNI PVNNKSVNVGFIGIVTKDIPNLV
RKNYEQYEFLEDEAETIVKYAKELQAKNVKAIIVLAHVAPATSKDDIAEGEAAEMMKVNL
FPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGGKAYADVRGVLDTDTQDFIETPSAKV
IAVAPGKKTGSADIQAIIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSPVGSGLITE
AQLAIARKSWPIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFNGILQVVEITGRDLY
KALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGBEINPDACYKLVIN
DFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVPNKPKIYVTMKNV
NETITQNDGTHSIIKKLYLDRQGNIVAQEIVSDTLNQTQKSKSTKINPVTTIHKKQLHQFTA

Table 71: Comparative Sequences relating to SAG1333

INPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7115

STRAIN H36B frame: 2

QVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAPD
 SNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEFLEDAETI VKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAE
 MMKKVNQLFPENSVDI VFAGHNHQYTNGLVGKTRI VQALSQKAYADVRGVLDTDQDFI
 ETPSAKVIAVAPGKKTGSADI QAI VQDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLI KPDGTITWGAAQAVQPPFNILQV
 EITGRDLYKALNEQYDQKQNFLLQIAGLRITYTDNKEGGEETPFKVVKAYKSNGEIINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVNNKPKI
 YVTMKNVNETITQNDGTYSI I KKL YLDRQGNIVAQEI VSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7116

STRAIN 18RS21 frame: 1

DQVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESI
 RVQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAP
 DSNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIV
 TKDI PNLVLRKNYEQYEFLEDAETI VKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAA
 EMMKKVNQLFPENSVDI VFAGHNHQYTNGLVGKTRI VQALSQKAYADVRGVLDTDQDFI
 IETPSAKVIAVAPGKKTGSADI QAI VQDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVS
 PVGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLI KPDGTITWGAAQAVQPPFNILQV
 VEITGRDLYKALNEQYDQKQNFLLQIAGLRITYTDNKEGGEETPFKVVKAYKSNGEIINPD
 DAKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVNNKPKI
 IYVTMKNVNETITQNDGTYSI I KKL YLDRQGNIVAQEI VSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKSK

SEQ ID NO. 7117

STRAIN M732 frame: 3

QVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAPD
 SNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEFLEDAETI VKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAE
 MMKKVNQLFPENSVDI VFAGHNHQYTNGLVGKTRI VQALSQKAYADVRGVLDTDQDFI
 ETPSAKVIAVAPGKKTGSADI QAI VQDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLI KPDGTITWGAAQAVQPPFNILQV
 EITGRDLYKALNEQYDQKQNFLLQIAGLRITYTDNKEGGEETPFKVVKAYKSNGEIINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVNNKPKI
 YVTMKNVNETITQNDGTYSI I KKL YLDRQGNIVAQEI VSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7118

STRAIN COH1 frame: 3

QVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAPD
 SNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEFLEDAETI VKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAE
 MMKKVNQLFPENSVDI VFAGHNHQYTNGLVGKTRI VQALSQKAYADVRGVLDTDQDFI
 ETPSAKVIAVAPGKKTGSADI QAI VQDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLI KPDGTITWGAAQAVQPPFNILQV
 EITGRDLYKALNEQYDQKQNFLLQIAGLRITYTDNKEGGEETPFKVVKAYKSNGEIINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVNNKPKI
 YVTMKNVNETITQNDGTYSI I KKL YLDRQGNIVAQEI VSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7119

STRAIN M781 frame: 1

QVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAPD
 SNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEFLEDAETI VKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAE
 MMKKVNQLFPENSVDI VFAGHNHQYTNGLVGKTRI VQALSQKAYADVRGVLDTDQDFI
 ETPSAKVIAVAPGKKTGSADI QAI VQDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLI KPDGTITWGAAQAVQPPFNILQV
 EITGRDLYKALNEQYDQKQNFLLQIAGLRITYTDNKEGGEETPFKVVKAYKSNGEIINPD
 AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVNNKPKI
 YVTMKNVNETITQNDGTYSI I KKL YLDRQGNIVAQEI VSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7120

STRAIN CJB110 frame: 1

DQVGQVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESI
 RVQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGNGHEFDEGLAEYNRIVTGKAPAP
 DSNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTI KNI PVNNKSVNVGFIGIV
 TKDI PNLVLRKNYEQYEFLEDAETI VKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAA
 EMMKKVNQLFPENSVDI VFAGHNHQYTNGLVGKTRI VQALSQKAYADVRGVLDTDQDFI
 IETPSAKVIAVAPGKKTGSADI QAI VQDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVS
 PVGSLITEAQLAIARKSWPDI DFAMTNNGGIRADLLI KPDGTITWGAAQAVQPPFNILQV
 VEITGRDLYKALNEQYDQKQNFLLQIAGLRITYTDNKEGGEETPFKVVKAYKSNGEIINPD

Table 71: Comparative Sequences relating to SAG1333

DAKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVPNKPK
IYVTMKNVNETITQNDGTHSIKKLYLDRQGNIVAQEI VSDTLNQTKSKSTKINPVTTIHK
KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7121

STRAIN 1169NT frame: 1

QVGQVIGVNDHFHGLDNTGTANMPDGKVNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
VQAGDMVGASPANSGLLQDEPTVKFNAMNVEYGTIGNHEFDEGLAEYNRI VTGKAPAPD
SNINNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYAIKNI PVNNKSVNVGFIGIVT
KDI PNVLVRKNYEQYEFLEDEATI VKYAKELQAKNVKAI VVLAHV PATSKND IAEGEAAE
MMKKVNQLFPENSVDI VFAGHNHQYTNGLVGKTRI VQALSQGKAYADVRGVLDTDQDFI
ETPSAKVIAVAPGKKTGSADI QAI VQDQANTIVKQVTEAKIGTAEVSMITRSVDQDNVSP
VGSILTEAQLAIARKSWPIDFAMTNNGGIRADLLIKPDGTITWGAQAQVQPFNGILQVV
EITGRDLKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKA YKSNGEI INPD
AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVPNKPKI
YVTMKNVNETITQNDGTHSIKKLYLDRQGNIVAQEI VSDTLNQTKSKSTKINPVTTIHK
KQLHQFTAINPMRNYGKPSNSTTVKS

SEQ ID NO. 7122

STRAIN JM9130013 frame: 2

GVQVIGVNDHFHGLDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRVQ
AGDMVGASPANSGLLQDEPTVKFNAMNVEYGTIGNHEFDEGLAEYNRI VTGKAPAPDSN
INNITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYTIKNI PVNNKSVNVGFIGIVTKD
IPNLVLRKNYEQYEFLEDEATI VKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAEM
KKVNQLFPENSVDI VFAGHNHQYTNGLVGKTRI VQALSQGKAYADVRGVLDTDQDFIET
PSAKVIAVAPGKKTGSADI QAI VQDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSPVG
SLITEAQLAIARKSWPIDFAMTNNGGIRADLLIKPDGTITWGAQAQVQPFNGILQVVEI
TGRDLKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKA YKSNGEI INPD
YKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKVSVPNKPKIYV
TMKNVNETITQNDGTHSIKKLYLDRQGNIVAQEI VSDTLNQTKSKSTKINPVTTIHKQ
LHQFTAINPMRNYGKPSNSTTVKS

PRETTY of: /biotmp/msa237615.2{*} May 14, 2003 03:22 ..

	i		50
msa237615.2{328_1169NT}	-----	-----qv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_2603}	mkkkilkss vlglvagtsi mfsavfaDqv	gvqvigVNDF	HGALDNTGTA
msa237615.2{328_A909}	-----	-----VNDF	HGALDNTGTA
msa237615.2{328_M732}	-----	-----qv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_COH1}	-----	-----qv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_M781}	-----	-----qv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_H36B}	-----	-----qv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_JM9130013}	-----	-----	gvqvigVNDF HGALDNTGTA
msa237615.2{328_18RS21}	-----	-----Dqv	gvqvigVNDF HGALDNTGTA
msa237615.2{328_090}	-----	-----v	gvqvigVNDF HGALDNTGTA
msa237615.2{328_CJB110}	-----	-----Dqv	gvqvigVNDF HGALDNTGTA
Consensus	*****	*****	*****
	51		100
msa237615.2{328_1169NT}	NMPDGKVaNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_2603}	NMPDGKVaNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_A909}	NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_M732}	NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_COH1}	NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_M781}	NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_H36B}	NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_JM9130013}	NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_18RS21}	NMPDGKVxNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_090}	NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
msa237615.2{328_CJB110}	NMPDGKVtNA GTAAQLDAYM DDAQKDFKQT	NPNGESIRVQ	AGDMVGASPA
Consensus	*****	*****	*****
	101		150
msa237615.2{328_1169NT}	NSGLLQDEPT VknFNAMNVE YGTIGNHEFD	EGLAEYNRIV	TGKAPAPDSN
msa237615.2{328_2603}	NSGLLQDEPT VknFNAMNVE YGTIGNHEFD	EGLAEYNRIV	TGKAPAPDSN
msa237615.2{328_A909}	NSGLLQDEPT VktFNAMNVE YGTIGNHEFD	EGLAEYNRIV	TGKAPAPDSN
msa237615.2{328_M732}	NSGLLQDEPT VktFNAMNVE YGTIGNHEFD	EGLAEYNRIV	TGKAPAPDSN
msa237615.2{328_COH1}	NSGLLQDEPT VktFNAMNVE YGTIGNHEFD	EGLAEYNRIV	TGKAPAPDSN
msa237615.2{328_M781}	NSGLLQDEPT VktFNAMNVE YGTIGNHEFD	EGLAEYNRIV	TGKAPAPDSN
msa237615.2{328_H36B}	NSGLLQDEPT VktFNAMNVE YGTIGNHEFD	EGLAEYNRIV	TGKAPAPDSN
msa237615.2{328_JM9130013}	NSGLLQDEPT VktFNAMNVE YGTIGNHEFD	EGLAEYNRIV	TGKAPAPDSN
msa237615.2{328_18RS21}	NSGLLQDEPT VktFNAMNVE YGTIGNHEFD	EGLAEYNRIV	TGKAPAPDSN
msa237615.2{328_090}	NSGLLQDEPT VktFNAMNVE YGTIGNHEFD	EGLAEYNRIV	TGKAPAPDSN
msa237615.2{328_CJB110}	NSGLLQDEPT VktFNAMNVE YGTIGNHEFD	EGLAEYNRIV	TGKAPAPDSN
Consensus	*****	*****	*****
	151		200
msa237615.2{328_1169NT}	INNITKSYPH EAAKQEI VVA NVIDKVNKQI	PYNWKPYaIK	NIPVNNKSVN
msa237615.2{328_2603}	INNITKSYPH EAAKQEI VVA NVIDKVNKQI	PYNWKPYaIK	NIPVNNKSVN
msa237615.2{328_A909}	INNITKSYPH EAAKQEI VVA NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_M732}	INNITKSYPH EAAKQEI VVA NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_COH1}	INNITKSYPH EAAKQEI VVA NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_M781}	INNITKSYPH EAAKQEI VVA NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN

Table 71: Comparative Sequences relating to SAG1333

msa237615.2{328_H36B}	INNITKSYPH	EAAKQEI VVA	NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_JM9130013}	INNITKSYPH	EAAKQEI VVA	NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_18RS21}	INNITKSYPH	EAAKQEI VVA	NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_090}	INNITKSYPH	EAAKQEI VVA	NVIDKVNKQI	PYNWKPYaIK	NIPVNNKSVN
msa237615.2{328_CJB110}	INNITKSYPH	EAAKQEI VVA	NVIDKVNKQI	PYNWKPYaIK	NIPVNNKSVN
Consensus	*****	*****	*****	*****-*	*****
msa237615.2{328_1169NT}	201				250
msa237615.2{328_2603}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_A909}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_M732}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_COH1}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_M781}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_H36B}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_JM9130013}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_18RS21}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_090}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_CJB110}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEAE	TIVKYAKELQ	AKNVKAI VVL
Consensus	*****	*****	*****	*****	*****
msa237615.2{328_1169NT}	251				300
msa237615.2{328_2603}	AHVPATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_A909}	AHVPATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_M732}	AHVPATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_COH1}	AHVPATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_M781}	AHVPATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_H36B}	AHVPATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_JM9130013}	AHVPATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_18RS21}	AHVPATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_090}	AHVPATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
msa237615.2{328_CJB110}	AHVPATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLVGK
Consensus	*****	*****	*****	*****	*****
msa237615.2{328_1169NT}	301				350
msa237615.2{328_2603}	TRIVQALSQG	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_A909}	TRIVQALSQG	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_M732}	TRIVQALSQG	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_COH1}	TRIVQALSQG	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_M781}	TRIVQALSQG	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_H36B}	TRIVQALSQG	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_JM9130013}	TRIVQALSQG	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_18RS21}	TRIVQALSQG	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_090}	TRIVQALSQG	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
msa237615.2{328_CJB110}	TRIVQALSQG	KAYADVRGVL	DTDTQDFIET	PSAKViAVAP	GKKTGSADIQ
Consensus	*****	*****	*****	*****	*****
msa237615.2{328_1169NT}	351				400
msa237615.2{328_2603}	AIVDQANTIV	KQVTEAKIGT	AEVSvMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_A909}	AIVDQANTIV	KQVTEAKIGT	AEVSvMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_M732}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_COH1}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_M781}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_H36B}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_JM9130013}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_18RS21}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_090}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_CJB110}	AIVDQANTIV	KQVTEAKIGT	AEVSgMITRS	VDQDNVSPVG	SLITEAQLAI
Consensus	*****	*****	*****	*****	*****
msa237615.2{328_1169NT}	401				450
msa237615.2{328_2603}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_A909}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_M732}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_COH1}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_M781}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_H36B}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_JM9130013}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_18RS21}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_090}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_CJB110}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
Consensus	*****	*****	*****	*****	*****
msa237615.2{328_1169NT}	451				500
msa237615.2{328_2603}	TGRDLYKALN	EQYDQKQNF	LQIAGLRITY	TDNKEGG EET	PFKVV KAYKS
msa237615.2{328_A909}	TGRDLYKALN	EQYDQKQNF	LQIAGLRITY	TDNKEGG EET	PFKVV KAYKS
msa237615.2{328_M732}	TGRDLYKALN	EQYDQKQNF	LQIAGLRITY	TDNKEGG EET	PFKVV KAYKS
msa237615.2{328_COH1}	TGRDLYKALN	EQYDQKQNF	LQIAGLRITY	TDNKEGG EET	PFKVV KAYKS

Table 71: Comparative Sequences relating to SAG1333

msa237615.2{328_M781}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_H36B}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_JM9130013}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_18RS21}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_090}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_CJB110}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
Consensus	*****	*****	*****	*****	*****
501					
msa237615.2{328_1169NT}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_2603}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_A909}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_M732}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_COH1}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_M781}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_H36B}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_JM9130013}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_18RS21}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_090}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_CJB110}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
Consensus	*****	*****	*****	*****	*****
551					
msa237615.2{328_1169NT}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_2603}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_A909}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_M732}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_COH1}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_M781}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_H36B}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_JM9130013}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_18RS21}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_090}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi
msa237615.2{328_CJB110}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIik	KLYLDRQGNi
Consensus	*****	*****	*****	*****	*****
601					
msa237615.2{328_1169NT}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_2603}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_A909}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_M732}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_COH1}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_M781}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_H36B}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_JM9130013}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_18RS21}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_090}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_CJB110}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
Consensus	*****	*****	*****	*****	*****
651					
msa237615.2{328_1169NT}	TVKS-----	-----	-----	-----	690
msa237615.2{328_2603}	TVKSKQlpkt	nseyggsflm	svfgvgligi	alntkklhmk	
msa237615.2{328_A909}	TVKSKQ----	-----	-----	-----	
msa237615.2{328_M732}	TVKSKQ----	-----	-----	-----	
msa237615.2{328_COH1}	TVKS-----	-----	-----	-----	
msa237615.2{328_M781}	TVKS-----	-----	-----	-----	
msa237615.2{328_H36B}	TVKS-----	-----	-----	-----	
msa237615.2{328_JM9130013}	TVKSK-----	-----	-----	-----	
msa237615.2{328_18RS21}	TVKSK-----	-----	-----	-----	
msa237615.2{328_090}	TVKSKQ----	-----	-----	-----	
msa237615.2{328_CJB110}	TVKS-----	-----	-----	-----	
Consensus	*****	*****	*****	*****	

Table 72: Comparative Sequences relating to SAG0941

SEQ ID NO. 7201

STRAIN 2603

ATGAATAAACCGGTAAAAATCGTTGCAACACTTGGTCCGCGGTTGAATTCGGTGGTG
 GTAAGAAGTTTGGTGAGTCTGGATACCTGGGGTGAAGCCTTGACGTAGAAGCTTCAGCAG
 AAAAAATTGCTCAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATG
 GAGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAGAGATTGCAG
 GACAAAAAGTTGGCTTCCCTCCTTGATACTAAAGGACCTGAAATTCGTACAGAAGCTTTTGG
 AAGATGGTGCAGATTTCCATTCAATATACAACAGGTACAAAAATTACGTGTTGCTACTAAGC
 AAGGTATCAAATCACTCCAGAAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCT
 TTGATGACGTTGAAGTTGGTAAGCAAATCCTTGTGATGATGGTAACTAGGTCTTACTG
 TGTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATGATGGCCCTTA
 TTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAATTCCTTTCCAGCACTTGCGAG
 AACCGGATAATGCTGATATCCGTTTGGACTTGAGCAAGGACTTAACCTTATTGCTATCT
 CATTTGTACGTACTGCTAAAGATGTTAATGAAGTTCGTGCTATTTTGTGAAGAACTGGsm
 ATGGACACGTTAAGTTGTTTCTAAATTTGAAATCAACAAGGTATCGATAATATTGATG
 AGATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTATCGAAGTTC
 CATTTGAAATGTTTCCAGTTTACCAAAAAATGATCATTAATAAGTTAATGCAGCTGGTA
 AAGCAGTTATTACAGCAACAAATATGCTTGAACAATGACTGATAAACCCAGTGCAGCTC
 GTTCAGAAGTATCTGATGCTTCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTT
 CAGTGAGTCAGCTAATGGTAAATACCCAGTTGAGTCAGTTGTAACAATGGCTACTATTG
 ATAAAAATGCTCAAACTATTACTCAATGAGTATGGTTCGCTTAGACTCTGCTATCCAC
 GTAATAACAAAACTGATGTTATTGCTATCTGCGTTAAAGATGCAACACACTCAATGGATA
 TCAAACTTGTGTTAACTACTGAAACAGGTAAATACAGCTCGTGCCATTCTTAAATCC
 GTCCAGATGCAACACTTTGGCTGTTACATTTGATGAAAAAGTACAACGTTCAATTGATGA
 TTAATCGGGTGTATCCCTGCTTGCAGACAAACAGCATCTACAGATGATATGTTTG
 AGGTTGCAGAAGCTGTAGCACTTGAAGCAGGATTGTTGAATCAGGCGATAATATCGTTA
 TCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACAAACAATGCGTGTTCGTACTGTTA
 AA

SEQ ID NO. 7202

STRAIN 090

AATAAACCGGTAAAAATCGTTGCAACACT
 TGGTCCGCGGTAGAATTCGGTGGTGAAGAAGTTTGGTGAGTCTGGAT
 ACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCTCAA
 TTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGGAGA
 TCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAGAGA
 TTGCAGGACAAAAAGTTGGCTTCCCTCCTTGATACTAAAGGACCTGAAAT
 CGTACAGAATTTTTGAAGATGGTTCAGATTTCCATTCAATATACAACAGG
 TACAGAATTACGTGTTGCTACTAAGCAAGGTATCAAATCACTCCAGAAG
 TGATTGCAATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTTGAA
 GTTGGTAAAGCAATCCTTGTGATGATGGTAACTAGGTCTTACTGTGTT
 TGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATGATG
 GCCTTATTGGTAAACAAAAAGGTGTAAACATCCCTTATACTAAATTCCT
 TTCCCAgCACTTGCAGAACCGGATAATGCTGATCCGTTTGGACTTGA
 GCAAGGACTTAACCTTTATTGCTATCTCATTGTGACGTACTGCTAAGATG
 TTAATGAAGTTCGTGCTATTGTTGAAGAACTGGCAATGGACATGTTAAG
 TTGTTTGCTAAATTTGAAATCAACAAGGTATCGATAATATTGATGAGAT
 TATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTATCG
 AAGTTCCTATTGAAATGGTCCAGTTTACCAAAAAATGATCAATTACTAAA
 GTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAATATGCTTGAAAC
 AATGACTGATAAACCCAGTGCAGCTCGTTCAGAAGTATCTGATGCTTCA
 ATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCCAGGTGAGTCAGCT
 AATGGTAAATACCCAGTTGAGTCAGTTGCTACAATGGCTACTATTGATAA
 AAATGCTCAAACATTACTCAATGAGTATGGTTCGCTTAGACTCATCTGCAT
 TCCCACTAATAACAAAACTGATGTTATTGCTATCTGCGGTTAAAGATGCA
 ACACACTCAATGGATATCAAACCTTGTGTGACAATTACTGAAACAGGTAA
 TACAGCTCGTGCCATTCTAAATTCGCTCCAGATGCAGACATTTTGGCTG
 TTACATTTGATGAAAAAGTACAACGTTTCAATTGATGATTAACTGGGGTGT
 ATCCCTGTCTTGCAGACAAACAGCATCTACAGATGATATGTTTGAGGT
 TGCAGAAGCTGTAGCACTTGAAGCAGGACTTGTGAATCAGGCGATAATA
 TCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACTAACACAATG
 CGTGTTCGTACTGTTAAA

SEQ ID NO. 7203

STRAIN A909

AATAAACCGGTAAAAATCGTTGCAACACTTGGTC
 CTGCGGTTGAATTCGGTGGTGAAGAAGTTTGGTGAGTCTGGATCTGG
 GGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCTCAATTGAT
 TAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGGAGATCATG
 CTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAGAGATTGCA
 GGACAAAAAGTTGGCTTCCCTCCTTGATACTAAAGGACCTGAAATTCGTAC
 AGAATTTTTGAAGATGGTGCAGATTTCCATTCAATATACAACAGGTACAA
 AATTACGTTGTTGCTACTAAGCAAGGTATCAAATCACTCCAGAAGTGATT
 GCAATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTTGAAGTTGG
 TAAGCAATCCTTGTGATGATGGTAACTAGGTCTTACTGTGTTTGCAA
 AAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATGATGGCCTT
 ATTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAAATTCCTTTCC
 AGCACTTGCAAGACCGGATAATGCTGATATCCGTTTGGACTTGAGCAAG
 GACTTAACCTTTATTGCTATCTCATTGTACGTACTGCTAAAGATGTTAAT
 GAAGTTTCGTGCTATTGTTGAAGAACTGGCAATGGACAGCTTAAGTTGTT
 TGCTAAAAATTTGAAATCAACAAGGTATCGATAATATTGATGAGATTATCG
 AAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTATCGAAGTT
 CCATTGAAATGTTCCAGTTTACCAAAAAATGATCATTAATAAGTTAA

Table 72: Comparative Sequences relating to SAG0941

TGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGAAACAATGA
 CTGATAAACCCAGTGCAGCTCGTTTCAGAGTATCTGATGTCTTCAATGCT
 GTTATTGATGGTACTGATGCTACAATGCTTTTCAGGTGAGTCAGCTAATGG
 TAAATACCCAGTTGAGTCAGTTCGTACATGGCTACTATTGATAAAAAATG
 CTCAAACATTACTCAATGAGTATGGTTCGCTTAGACTCATCTGCATTCCCA
 CGTAATAACAAAACTGATGTTATTGCACTCGCGTTAAAGATGCAACACA
 CTCATGGATATCAAACTTGTGTAAACATTACTGAAACAGGTAATACAG
 CTGTCGCCATTCTTAAATTCGGTCCAGATGCAGACATTTTGGCTGTTACA
 TTTGATGAAAAAGTACAACGTTTCATTGATGATTAACTGGGGTGTATCCC
 TGTCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGGAGTTGCAG
 AACGTGTAGCACTTGAAGCAGGATTGTTGAATCAGGCGATAATATCGTT
 ATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACCTAACCAATGCGTGT
 TCGTACTGTAAA

SEQ ID NO. 7204

STRAIN H36B

AATAAACGCGTAAAAATCGTTGCAAC
 ACTTGGTCTCGCGTTGAATTCGGTGGTGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCATATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAG
 AGATTGCAAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAA
 ATTTCGTACAGAACTTTTGAAGATGGTGCAGATTTCCATTATATACAAC
 AGGTACAAAAATTACGTGTTGCTACTAAGCAAGGTATCAAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAAGGTGTAAACATCCCTTATACTAAAAAT
 CCTTTCCAGCACTTGCAAGAACGCGATAATGCTGATATCCGTTTGGACT
 TGAGCAAGGACTTAACCTTTATTGCTATCTCATTGTGACGTACTGCTAAG
 ATGTTAATGAAGTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGTCTAAAAATGAAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCCATTGAAATGGTTCAGTTTACCAAAAAATGATCAITACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACACAGTGCAGACTCGTTGAGAAGTATCTGATGTCT
 TCAATGCTGTTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAAATGGCTACTATTGA
 TAAAAATGCTCAAAACATTACTCAATGAGTATGGTTCGCTTAGACTCATCTG
 CATTCACGCTAATAACAAAACTGATGTTATTGCACTCGCGTTAAAGAT
 GCAACACACTCAATGGATATCAAACTTGTGTAAACATTACTGAAACAGG
 TAATACAGCTCGTGCCATTCTTAAATTCGGTCCAGATGCAGACATTTTGG
 CTGTTACATTGATGAAAAAGTACAACGTTTCATTGATGATTAACTGGGGT
 GTTATCCCTGTCCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
 GGTTGCAGAACGTGTAGCACTTGAAGCAGGATTGTTGAATCAGGCGATA
 ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACCTAACACA
 ATGCGTGTTCGTACTGTAAA

SEQ ID NO. 7205

STRAIN 18RS21

AATAAACGCGTAAAAATCGTTGCAAC
 ACTTGGTCTCGCGTTGAATTCGGTGGTGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCATATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAG
 AGATTGCAAGGACAAAAAGTTGGCTTCCTCCTTGATACTAAAGGACCTGAA
 ATTCGTACAGAACTTTTGAAGATGGTGCAGATTTCCATTATATACAAC
 AGGTACAAAAATTACGTGTTGCTACTAAGCAAGGTATCAAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAAGGTGTAAACATCCCTTATACTAAAAAT
 CCTTTCCAGCACTTGCAAGAACGCGATAATGCTGATATCCGTTTGGACT
 TGAGCAAGGACTTAACCTTTATTGCTATCTCATTGTGACGTACTGCTAAG
 ATGTTAATGAAGTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGTCTAAAAATGAAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCCATTGAAATGGTTCAGTTTACCAAAAAATGATCAITACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACACAGTGCAGACTCGTTGAGAAGTATCTGATGTCT
 TCAATGCTGTTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTGA
 TAAAAATGCTCAAAACATTACTCAATGAGTATGGTTCGCTTAGACTCATCTG
 CATTCACGCTAATAACAAAACTGATGTTATTGCACTCGCGTTAAAGAT
 GCAACACACTCAATGGATATCAAACTTGTGTAAACATTACTGAAACAGG
 TAATACAGCTCGTGCCATTCTTAAATTCGGTCCAGATGCAGACATTTTGG
 CTGTTACATTGATGAAAAAGTACAACGTTTCATTGATGATTAACTGGGGT
 GTTATCCCTGTCCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
 GGTTGCAGAACGTGTAGCACTTGAAGCAGGATTGTTGAATCAGGCGATA
 ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACCTAACACA
 ATGCGTGTTCGTACTGTAAA

SEQ ID NO. 7206

Table 72: Comparative Sequences relating to SAG0941

STRAIN M732

AATAAACGCGTAAAAATCGTTGCAAC
 ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATATAAAGGACCTGAA
 ATTCGTACAGAACTTTTGAAGATGGTGCAGATTCCATTATATACAAC
 AGGTACAAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAAAT
 CCTTTCCAGCACTTGCGAAGCGGATAATGCTGATATCCGTTTTGGACT
 TGAGCAAGGACTTAACCTTTATGCTATCTCATTGTACGTACTGCTAAAG
 ATGTTAATGAAGTTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGCTAAAAATTGAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTATATGGGTA
 TCGAAGTTCCATTGAAATGGTTCAGTTTACCAAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAACTGACTGATAAACCCAGTGCAGCTCGTTGAGATATCTGATGTCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTTCGTACAATGGCTACTATTGA
 TAAAAATGCTCAAACTTACTCAATGAGTATGGTTCGCTTAGACTCATCTG
 CATTTCCACGTAATAACAAAACTGATGTTATTGCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACTTGTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAATTCGGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTTCAATGATGATTAACTGGGGT
 GTTATCCCTGTCTTGCAGACAAACCAGCATCTACAGATGATATGTTGA
 GGTTCGAGAACGTGTAGCACTTGAAGCAGGACTTGTGTAATCAGGCGATA
 ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACCTAACACA
 ATGCGTGTTCGTACTGTTAA

SEQ ID NO. 7207

STRAIN COH1

AATAAACGCGTAAAAATCGTTGCAAC
 ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATATAAAGGACCTGAA
 ATTCGTACAGAACTTTTGAAGATGGTGCAGATTCCATTATATACAAC
 AGGTACAAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATGTTAAACAAAAAGGTGTAACATCCCTTATACTAAAAAT
 CCTTTCCAGCACTTGCGAAGCGGATAATGCTGATATCCGTTTTGGACT
 TGAGCAAGGACTTAACCTTTATGCTATCTCATTGTACGTACTGCTAAAG
 ATGTTAATGAAGTTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGCTAAAAATTGAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTATATGGGTA
 TCGAAGTTCCATTGAAATGGTTCAGTTTACCAAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAACTGACTGATAAACCCAGTGCAGCTCGTTGAGATATCTGATGTCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTTCGTACAATGGCTACTATTGA
 TAAAAATGCTCAAACTTACTCAATGAGTATGGTTCGCTTAGACTCATCTG
 CATTTCCACGTAATAACAAAACTGATGTTATTGCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACTTGTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAATTCGGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTTCAATGATGATTAACTGGGGT
 GTTATCCCTGTCTTGCAGACAAACCAGCATCTACAGATGATATGTTGA
 GGTTCGAGAACGTGTAGCACTTGAAGCAGGACTTGTGTAATCAGGCGATA
 ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACCTAACACA
 ATGCGTGTTCGTACTGTTAA

SEQ ID NO. 7208

STRAIN M781

AATAAACGCGTAAAAATCGTTGCAAC
 ACTTGGTCCTGCGGTAGAATTCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCCTCCTTGATATAAAGGACCTGAA
 ATTCGTACAGAACTTTTGAAGATGGTGCAGATTCCATTATATACAAC
 AGGTACAAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAAAT
 CCTTTCCAGCACTTGCGAAGCGGATAATGCTGATATCCGTTTTGGACT
 TGAGCAAGGACTTAACCTTTATGCTATCTCATTGTACGTACTGCTAAAG

Table 72: Comparative Sequences relating to SAG0941

ATGTTAATGAAGTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGCTAAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCATTGAAATGGTTCAGTTTACCAAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACCCAGTGGGACTCGTTCAGAAGTATCTGATGCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTGCTACAATGGCTACTATTGA
 TAAAAATGCTCAAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTTCCACGTAATAACAAACTGATGTTATTGTCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACTTGTGTAAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAGTTCGGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTCAITGATGATTAACTGGGGT
 GTTATCCCTGTCCTTGAGACAAACAGCATCTACAGATGATATGTTTGA
 GGTTCAGAACGTTGAGCACTTGAAGCAGGACTTGTGAATCAGGCGATA
 ATATCGTTATCGTTGAGGTGTTCTGTAGGTACAGGTGGAACATAACACA
 ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7209

STRAIN CJB110

AATAAACCGGTAAAAATCGTTGCAAC
 ACTTGGTCTCGCGTTGAATTCGGTGGTGAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCGGTTTCAACTTCTCATATGG
 AGATCATGCTGAGCAAGCAGCTCGTATGGCTACTGTTTCTGTAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCTCTTGTATCTAAAGGACCTGAA
 ATTCTGACAGAACTTTTGAAGATGGTGCAGATTCCATTCTATATACAAC
 AGGTACAAAATTACGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAATT
 CCTTTCCAGCACTTGCAGAACGCGATAATGCTGATATCCGTTTGGACT
 TGAACAAGGACTTAACTTTATTGCTATCTCATTTGTACGTACTGCTAAAG
 ATGTTAATGAAGTTTCTGCTATTTGTGAAGAACTGGCAATGGACAGTT
 AAGTTGTTTGTAAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCATTGAAATGGTTCAGTTTACCAAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACCCAGTGGGACTCGTTCAGAAGTATCTGATGCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTGCTACAATGGCTACTATTGA
 TAAAAATGCTCAAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTTCCACGTAATAACAAACTGATGTTATTGTCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACTTGTGTAAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAATTCGGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTCAITGATGATTAACTGGGGT
 GTTATCCCTGTCCTTGAGACAAACAGCATCTACAGATGATATGTTTGA
 GGTTCAGAACGTTGAGCACTTGAAGCAGGACTTGTGAATCAGGCGATA
 ATATCGTATATCGTTGAGGTGTTCTGTAGGTACAGGTGGAACATAACACA
 ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7210

STRAIN 1169NT

AATAAACCGGTAAAAATCGTTGCAAC
 ACTTGGTCTCGCGTGAAGTTCCGGTGGTGAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTTCGGTTTCAACTTCTCATATGG
 AGATCATGCTGAGCAAGCAGCTCGTATGGCTACTGTTTCTGTAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCTCTTGTATCTAAAGGACCTGAA
 ATTCTGACAGAACTTTTGAAGATGGTGCAGATTCCATTCTATATACAAC
 AGGTACAAAATTACGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAATT
 CCTTTCCAGCACTTGCAGAACGCGATAATGCTGATATCCGTTTGGACT
 TGAGCAAGGACTTAACTTTATTGCTATCTCATTTGTACGTACTGCTAAAG
 ATGTTAATGAAGTTTCTGCTATTTGTGAAGAACTGGCAATGGACAGTT
 AAGTTGTTTGTAAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
 TCGAAGTTCATTGAAATGGTTCAGTTTACCAAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACCCAGTGGGACTCGTTCAGAAGTATCTGATGCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTGCTACAATGGCTACTATTGA
 TAAAAATGCTCAAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTTCCACGTAATAACAAACTGATGTTATTGTCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACTTGTGTAAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAATTCGGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTCAITGATGATTAACTGGGGT
 GTTATCCCTGTCCTTGAGACAAACAGCATCTACAGATGATATGTTTGA
 GGTTCAGAACGTTGAGCACTTGAAGCAGGACTTGTGAATCAGGCGATA
 ATATCGTATATCGTTGAGGTGTTCTGTAGGTACAGGTGGAACATAACACA
 ATGCGTGTTCGTACTGTTAAA

Table 72: Comparative Sequences relating to SAG0941

ATATCGTTATCGTTGCAGGTGTTCTCTGTAGGTACAGGTGGAACCTAACACA
ATGCGTGTTCGTACTGTTAA

SEQ ID NO. 7211

STRAIN JM9130013

AATAAACCGGTAAAAATCGTTGCAAC

ACTTGGTCTCGCGGTAGAAATCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
GATACCTGGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
CAATTGATTAAAGAAGGTGCTAACGTTTTCCTGTTCAACTTCTCACATGG
AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTCTGTAAGCAGAAG
AGATTGCAGGACAAAAAGTTGGCTTCTCTCTGATACTAAAGGACCTGAA
ATTCGTACAGAACTTTTGAAGATGGTTTCAGATTTCCATTCATATACAA
AGGTACAAAAATTACGTGTTGCTACTAAGCAAGGTATCAATCAACTCCAG
AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
GAAGTTGGTAAGCAAAATCCTTGTGTGATGATGTTAACTAGGTCTTACTGT
GTTTGCAGAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
ATGGCCTTATTTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAAAT
CCTTTCCAGCACTTGCAGAACGCGATAATGCTGATATCCGTTTGGACT
TGAGCAAGGACTTAACCTTTATTGCTATCTCATTTGTACGTACTGCTAAAG
ATGTTAATGAAGTTTCTGCTATTGTTGTAAGAACTGGCAATGGACATGTT
AAGTTGTTTGTCTAAATTTGAATAACCAAGGTATCGATAATATTGATGA
GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGATATGGGTA
TCGAAGTTCCATTTGAAATGGTTCCAGTTTACCAAAAAATGATCATTACT
AAAGTTAATGCAAGCTGGTAAAGCAGTTATACAGCAACAAATATGCTTGA
AACAACTGACTGATAAACCCAGTGCAGCTCGTTTCAAGATATCTGATGCT
TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
GCTAATGGTAAATACCCAGTTGAGTCACTTCTGTAATGGCTACTATTGA
TAAAAATGCTCAACATTACTCAATGAGTATGGTTCGCTTAGACTCATCTG
CATTTCCAGCTAATAACAAAACTGATGTTATGCACTCTGCGGTTAAAGAT
GCAACCACTCAATGGATATCAAACTTGTGTGACAATTACTGAAACAGG
TAATACAGCTCGTGCCATTTCTAAATCCGTCAGATGCAGACATTTTGG
CTGTTACATTTGATGAAAAAGTACACGTTTATTGATGATTAACTGGGGT
GTATCTCTGCTGCTGCAAGAACAGCATCTACAGATGATATGTTTGA
GGTTGCAGAACGTTAGcACTTGAAGCAGGACTTGTGAATCAGGCGATA
ATATCGTTATCGTTGCAGGTGTTCTCTGTAGGTACAGGTGGAACCTAACACA
ATGCGTGTTCGTACTGTTAA

PRETTY of: /biotmp/msa277466.2{*} February 24, 2003 01:44 ..

	1		50
msa277466.2{330_090}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_JM9130013}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_18RS21}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_2603}	atgAATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_A909}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_H36B}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_CJB110}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_COH1}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_M732}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_1169NT}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
msa277466.2{330_M781}	---AATAAAC	GCGTAAAAAT	CGTTGCAACA
Consensus	*****	*****	*****
	51		100
msa277466.2{330_090}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_JM9130013}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_18RS21}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_2603}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_A909}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_H36B}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_CJB110}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_COH1}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_M732}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_1169NT}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
msa277466.2{330_M781}	CCGTGGTGGT	AAGAAGTTTG	GTGAGTCTGG
Consensus	*****	*****	*****
	101		150
msa277466.2{330_090}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_JM9130013}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_18RS21}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_2603}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_A909}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_H36B}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_CJB110}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_COH1}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_M732}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_1169NT}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
msa277466.2{330_M781}	ACGTAGAAGC	TTCAGCAGAA	AAAATTGCTC
Consensus	*****	*****	*****
	151		200
msa277466.2{330_090}	AACGTTTTTC	GTTTCAACTT	CTCACATGGA

Table 72: Comparative Sequences relating to SAG0941

msa277466.2{330_JM9130013}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_18RS21}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_2603}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_A909}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_H36B}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_CJB110}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_COH1}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_M732}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_1169NT}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_M781}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_JM9130013}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_18RS21}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_2603}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_A909}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_H36B}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_CJB110}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_COH1}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_M732}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_1169NT}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_M781}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_JM9130013}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_18RS21}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_2603}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_A909}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_H36B}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_CJB110}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_COH1}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_M732}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_1169NT}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_M781}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	GATGGTtCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_JM9130013}	GATGGTtCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_18RS21}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_2603}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_A909}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_H36B}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_CJB110}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_COH1}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_M732}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_1169NT}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_M781}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
Consensus	*****_***	*****	*****	*****_***	*****
msa277466.2{330_090}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_JM9130013}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_18RS21}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_2603}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_A909}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_H36B}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_CJB110}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_COH1}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_M732}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_1169NT}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_M781}	TACTAAGCAA	GGTATCAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_JM9130013}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_18RS21}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_2603}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_A909}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_H36B}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_CJB110}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_COH1}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_M732}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_1169NT}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_M781}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
Consensus	*****	*****	*****	*****	*****

451

500

Table 72: Comparative Sequences relating to SAG0941

msa277466.2{330_090}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_JM9130013}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_18RS21}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_2603}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_A909}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_H36B}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_CJB110}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_COH1}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_M732}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_1169NT}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_M781}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAAG	ATAAAGACAC
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_JM9130013}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_18RS21}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_2603}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_A909}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_H36B}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_CJB110}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_COH1}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_M732}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_1169NT}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_M781}	TCGTGAATTT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACGAG	ACTTGCAGAA
msa277466.2{330_JM9130013}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACGAG	ACTTGCAGAA
msa277466.2{330_18RS21}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACGAG	ACTTGCAGAA
msa277466.2{330_2603}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACGAG	ACTTGCAGAA
msa277466.2{330_A909}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACGAG	ACTTGCAGAA
msa277466.2{330_H36B}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACGAG	ACTTGCAGAA
msa277466.2{330_CJB110}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACGAG	ACTTGCAGAA
msa277466.2{330_COH1}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACGAG	ACTTGCAGAA
msa277466.2{330_M732}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACGAG	ACTTGCAGAA
msa277466.2{330_1169NT}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACGAG	ACTTGCAGAA
msa277466.2{330_M781}	AAGGTGTAAA	CATCCCTTAT	ACTAAATTC	CITTCACGAG	ACTTGCAGAA
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_JM9130013}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_18RS21}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_2603}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_A909}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_H36B}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_CJB110}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_COH1}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_M732}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_1169NT}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
msa277466.2{330_M781}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAGCAAGGAC	TTAACTTTAT
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_JM9130013}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_18RS21}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_2603}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_A909}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_H36B}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_CJB110}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_COH1}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_M732}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_1169NT}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
msa277466.2{330_M781}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTTCGTGCTA
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	TTTGTGAAGA	AAC TGGcaAT	GGACatGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_JM9130013}	TTTGTGAAGA	AAC TGGcaAT	GGACatGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_18RS21}	TTTGTGAAGA	AAC TGGcaAT	GGACacGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_2603}	TTTGTGAAGA	AAC TGGsmAT	GGACacGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_A909}	TTTGTGAAGA	AAC TGGcaAT	GGACacGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_H36B}	TTTGTGAAGA	AAC TGGcaAT	GGACacGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_CJB110}	TTTGTGAAGA	AAC TGGcaAT	GGACacGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_COH1}	TTTGTGAAGA	AAC TGGcaAT	GGACacGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_M732}	TTTGTGAAGA	AAC TGGcaAT	GGACacGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_1169NT}	TTTGTGAAGA	AAC TGGcaAT	GGACacGTTA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_M781}	TTTGTGAAGA	AAC TGGcaAT	GGACacGTTA	AGTTGTTTGC	TAAAATTGAA
Consensus	*****	*****	*****	*****	*****

Table 72: Comparative Sequences relating to SAG0941

		751					800
msa277466.2{330_090}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_JM9130013}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_18RS21}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_2603}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_A909}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_H36B}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_CJB110}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_COH1}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_M732}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_1169NT}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
msa277466.2{330_M781}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG		
Consensus	*****	*****	*****	*****	*****		
		801					850
msa277466.2{330_090}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_JM9130013}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_18RS21}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_2603}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_A909}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_H36B}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_CJB110}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_COH1}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_M732}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_1169NT}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
msa277466.2{330_M781}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAGTTCCA	TTTGAAATGG		
Consensus	*****	*****	*****	*****	*****		
		851					900
msa277466.2{330_090}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_JM9130013}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_18RS21}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_2603}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_A909}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_H36B}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_CJB110}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_COH1}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_M732}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_1169NT}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
msa277466.2{330_M781}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA		
Consensus	*****	*****	*****	*****	*****		
		901					950
msa277466.2{330_090}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_JM9130013}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_18RS21}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_2603}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_A909}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_H36B}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_CJB110}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_COH1}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_M732}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_1169NT}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
msa277466.2{330_M781}	GCAGTTATTA	CAGCAACAAA	TATGCTTGAA	ACAATGACTG	ATAAACCCAG		
Consensus	*****	*****	*****	*****	*****		
		951					1000
msa277466.2{330_090}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_JM9130013}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_18RS21}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_2603}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_A909}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_H36B}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_CJB110}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_COH1}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_M732}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_1169NT}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
msa277466.2{330_M781}	TGCGACTCGT	TCAGAAGTAT	CTGATGCTCT	CAATGCTGTT	ATTGATGGTA		
Consensus	*****	*****	*****	*****	*****		
		1001					1050
msa277466.2{330_090}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_JM9130013}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_18RS21}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_2603}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_A909}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_H36B}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_CJB110}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_COH1}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_M732}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_1169NT}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
msa277466.2{330_M781}	CTGATGCTAC	AATGCTTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT		
Consensus	*****	*****	*****	*****	*****		

Table 72: Comparative Sequences relating to SAG0941

		1051			1100
msa277466.2{330_090}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_JM9130013}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_18RS21}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_2603}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_A909}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_H36B}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_CJB110}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_COH1}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_M732}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_1169NT}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
msa277466.2{330_M781}		GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC
Consensus		*****	*****	*****	*****
		1101			1150
msa277466.2{330_090}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_JM9130013}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_18RS21}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_2603}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_A909}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_H36B}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_CJB110}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_COH1}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_M732}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_1169NT}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
msa277466.2{330_M781}		CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT
Consensus		*****	*****	*****	*****
		1151			1200
msa277466.2{330_090}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_JM9130013}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_18RS21}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_2603}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_A909}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_H36B}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_CJB110}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_COH1}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_M732}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_1169NT}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
msa277466.2{330_M781}		CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC
Consensus		*****	*****	*****	*****
		1201			1250
msa277466.2{330_090}		AAACTTGTG	TgACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_JM9130013}		AAACTTGTG	TgACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_18RS21}		AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_2603}		AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_A909}		AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_H36B}		AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_CJB110}		AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_COH1}		AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_M732}		AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_1169NT}		AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
msa277466.2{330_M781}		AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC
Consensus		*****	*****	*****	*****
		1251			1300
msa277466.2{330_090}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_JM9130013}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_18RS21}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_2603}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_A909}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_H36B}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_CJB110}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_COH1}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_M732}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_1169NT}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
msa277466.2{330_M781}		TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT
Consensus		***-*****	*****	*****	*****
		1301			1350
msa277466.2{330_090}		TACAACGTTT	ATTGATGATT	AAC TGGGGTG	TTATCCCTGT
msa277466.2{330_JM9130013}		TACAACGTTT	ATTGATGATT	AAC TGGGGTG	TTATCCCTGT
msa277466.2{330_18RS21}		TACAACGTTT	ATTGATGATT	AAC TGGGGTG	TTATCCCTGT
msa277466.2{330_2603}		TACAACGTTT	ATTGATGATT	AAC TGGGGTG	TTATCCCTGT
msa277466.2{330_A909}		TACAACGTTT	ATTGATGATT	AAC TGGGGTG	TTATCCCTGT
msa277466.2{330_H36B}		TACAACGTTT	ATTGATGATT	AAC TGGGGTG	TTATCCCTGT
msa277466.2{330_CJB110}		TACAACGTTT	ATTGATGATT	AAC TGGGGTG	TTATCCCTGT
msa277466.2{330_COH1}		TACAACGTTT	ATTGATGATT	AAC TGGGGTG	TTATCCCTGT
msa277466.2{330_M732}		TACAACGTTT	ATTGATGATT	AAC TGGGGTG	TTATCCCTGT
msa277466.2{330_1169NT}		TACAACGTTT	ATTGATGATT	AAC TGGGGTG	TTATCCCTGT
msa277466.2{330_M781}		TACAACGTTT	ATTGATGATT	AAC TGGGGTG	TTATCCCTGT

Table 72: Comparative Sequences relating to SAG0941

Consensus	*****	*****	*****	*****	*****
	1351				1400
msa277466.2{330_090}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_JM9130013}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_18RS21}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_2603}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_A909}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_H36B}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_CJB110}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_COH1}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_M732}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_1169NT}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_M781}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
Consensus	*****	*****	*****	*****	*****
	1401				1450
msa277466.2{330_090}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_JM9130013}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_18RS21}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_2603}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_A909}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_H36B}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_CJB110}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_COH1}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_M732}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_1169NT}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_M781}	TGAAGCAGGA	CTTGTGTAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
Consensus	*****	*****	*****	*****	*****
	1451				1500
msa277466.2{330_090}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_JM9130013}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_18RS21}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_2603}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_A909}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_H36B}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_CJB110}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_COH1}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_M732}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_1169NT}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_M781}	TTCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
Consensus	*****	*****	*****	*****	*****

SEQ ID NO. 7212

STRAIN 2603 frame: 1

MNKRKIVATLGPVAFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHG
 DHAEQGARMATVRKAEIAGQKVGFLDITKGPEIRTELFEDGADFHSYTTGTCLRVATKQ
 GKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGITVFAKDKDTREFEVVENDGLI
 GKQGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGX
 GHVKLFAKIEHQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGK
 AVITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATID
 KNAQTLLNEYGRDLSSAFPRNNKTDVIAVAVKDATHSMDIKLVVTTITETGNTARAI SKFRP
 PDADILAVTFDEKVRQSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNI VIV
 VAGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7213

STRAIN 090 frame: 1

NKRKIVATLGPVAFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEIAGQKVGFLDITKGPEIRTELFEDGADFHSYTTGTCLRVATKQ
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGITVFAKDKDTREFEVVENDGLI
 KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFKIEHQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDLSSAFPRNNKTDVIAVAVKDATHSMDIKLVVTTITETGNTARAI SKFRP
 DADILAVTFDEKVRQSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNI VIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7214

STRAIN A909 frame: 1

NKRKIVATLGPVAFRGGKKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEIAGQKVGFLDITKGPEIRTELFEDGADFHSYTTGTCLRVATKQ
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGITVFAKDKDTREFEVVENDGLI
 KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFKIEHQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDLSSAFPRNNKTDVIAVAVKDATHSMDIKLVVTTITETGNTARAI SKFRP
 DADILAVTFDEKVRQSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNI VIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7215

STRAIN H36B frame: 1

Table 72: Comparative Sequences relating to SAG0941

NKRVKIVATLGPVAFRGGKKFGESEGYWGESLDVEASAEDIAQLIKEGANVFRNFHSHGD
 HAEQGARMATVRKAEIAGQKVGFLDLTKGPEIRTELFDGADFHSTTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
 KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDLSSAFPRNNKTDVIA SAVKDATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFVAERVALEAGFVESGDNI VIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7216

STRAIN 18RS21 frame: 1

NKRVKIVATLGPVAFRGGKKFGESEGYWGESLDVEASAEDIAQLIKEGANVFRNFHSHGD
 HAEQGARMATVRKAEIAGQKVGFLDLTKGPEIRTELFDGADFHSTTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
 KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDLSSAFPRNNKTDVIA SAVKDATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFVAERVALEAGFVESGDNI VIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7217

STRAIN M732 frame: 1

NKRVKIVATLGPVAFRGGKKFGESEGYWGESLDVEASAEDIAQLIKEGANVFRNFHSHGD
 HAEQGARMATVRKAEIAGQKVGFLDLTKGPEIRTELFDGADFHSTTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
 KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDLSSAFPRNNKTDVIA SAVKDATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFVAERVALEAGFVESGDNI VIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7218

STRAIN COH1 frame: 1

NKRVKIVATLGPVAFRGGKKFGESEGYWGESLDVEASAEDIAQLIKEGANVFRNFHSHGD
 HAEQGARMATVRKAEIAGQKVGFLDLTKGPEIRTELFDGADFHSTTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
 KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDLSSAFPRNNKTDVIA SAVKDATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFVAERVALEAGFVESGDNI VIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7219

STRAIN M781 frame: 1

NKRVKIVATLGPVAFRGGKKFGESEGYWGESLDVEASAEDIAQLIKEGANVFRNFHSHGD
 HAEQGARMATVRKAEIAGQKVGFLDLTKGPEIRTELFDGADFHSTTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
 KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDLSSAFPRNNKTDVIA SAVKDATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFVAERVALEAGFVESGDNI VIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7220

STRAIN CJB110 frame: 1

NKRVKIVATLGPVAFRGGKKFGESEGYWGESLDVEASAEDIAQLIKEGANVFRNFHSHGD
 HAEQGARMATVRKAEIAGQKVGFLDLTKGPEIRTELFDGADFHSTTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
 KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDLSSAFPRNNKTDVIA SAVKDATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFVAERVALEAGFVESGDNI VIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7221

STRAIN 1169NT frame: 1

NKRVKIVATLGPVAFRGGKKFGESEGYWGESLDVEASAEDIAQLIKEGANVFRNFHSHGD
 HAEQGARMATVRKAEIAGQKVGFLDLTKGPEIRTELFDGADFHSTTTGKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
 KQKGVNI PYTKI PFPALAEARNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKIENQQGIDNIDEI IEAADGIMIARGDMGIEVPFEMVVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRDLSSAFPRNNKTDVIA SAVKDATHSMDIKLVVTITETGNTARAI SKFRP
 DADILAVTFDEKVQSRSLMINWGVIPVLADKPASTDDMFVAERVALEAGFVESGDNI VIV
 AGVPVGTGGTNTMRVRTVK

Table 72: Comparative Sequences relating to SAG0941

SEQ ID NO. 7222

STRAIN JM9130013 frame: 1

NKRVKIVATLGPVAFRGGKFGESGYWGESLDVEASAEKIAQLIKEGANVFRNFHSHG
 HAEQGMATVRKAEIAGQKVGFLDITKGPETELFEDGSDHFSYTTCTKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGITVFAKDKDTREFEVVENDGLIG
 KQKGVNIPYTKIPFPALAEADNADIRFGLGGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFKAIENQOQIDNIDEIIEAADGIMIAARGDMGIEVFPFMPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVDFNVIDGTDATMLSGESANGKYPVESVTRMATIDK
 NAQTLLENGRLDSSAFPRNKTVDIASAVKDATHSMDIKLVVTTITETGTARAIKFRP
 DADILAVTFDEKVRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIIVIV
 AGVPVGTGGTNTMRVRTVK

PRETTY of: /biotmp/msa277662.2{*} February 24, 2003 01:49 ..

msa277662.2{330_18RS21}	1	~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	50
msa277662.2{330_A909}		~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_CJB110}		~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_H36B}		~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_1169NT}		~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_COH1}		~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_M732}		~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_M781}		~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_JM9130013}		~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_090}		~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_2603}		~NKRVKIVAT	LGPVAFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
Consensus		*****	*****	*****	*****	*****	
msa277662.2{330_18RS21}	51	NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDITK	GPEIRTELFE	100
msa277662.2{330_A909}		NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDITK	GPEIRTELFE	
msa277662.2{330_CJB110}		NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDITK	GPEIRTELFE	
msa277662.2{330_H36B}		NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDITK	GPEIRTELFE	
msa277662.2{330_1169NT}		NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDITK	GPEIRTELFE	
msa277662.2{330_COH1}		NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDITK	GPEIRTELFE	
msa277662.2{330_M732}		NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDITK	GPEIRTELFE	
msa277662.2{330_M781}		NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDITK	GPEIRTELFE	
msa277662.2{330_JM9130013}		NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDITK	GPEIRTELFE	
msa277662.2{330_090}		NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDITK	GPEIRTELFE	
msa277662.2{330_2603}		NVFRNFHSHG	DHAEQGARMA	TVRKAEEIAG	QKVGFLDITK	GPEIRTELFE	
Consensus		*****	*****	*****	*****	*****	
msa277662.2{330_18RS21}	101	DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL	150
msa277662.2{330_A909}		DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL	
msa277662.2{330_CJB110}		DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL	
msa277662.2{330_H36B}		DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL	
msa277662.2{330_1169NT}		DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL	
msa277662.2{330_COH1}		DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL	
msa277662.2{330_M732}		DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL	
msa277662.2{330_M781}		DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL	
msa277662.2{330_JM9130013}		DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL	
msa277662.2{330_090}		DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL	
msa277662.2{330_2603}		DGADFHSYTT	GTKLRVATKQ	GIKSTPEVIA	LNAGGLDIF	DDVEVGKQIL	
Consensus		**~*****	**~*****	*****	*****	*****	
msa277662.2{330_18RS21}	151	VDDGKLGITV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE	200
msa277662.2{330_A909}		VDDGKLGITV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_CJB110}		VDDGKLGITV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_H36B}		VDDGKLGITV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_1169NT}		VDDGKLGITV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_COH1}		VDDGKLGITV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_M732}		VDDGKLGITV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_M781}		VDDGKLGITV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_JM9130013}		VDDGKLGITV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_090}		VDDGKLGITV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_2603}		VDDGKLGITV	FAKDKDTREF	EVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
Consensus		*****	*****	*****	*****	*****	
msa277662.2{330_18RS21}	201	RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKAKIE	250
msa277662.2{330_A909}		RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKAKIE	
msa277662.2{330_CJB110}		RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKAKIE	
msa277662.2{330_H36B}		RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKAKIE	
msa277662.2{330_1169NT}		RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKAKIE	
msa277662.2{330_COH1}		RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKAKIE	
msa277662.2{330_M732}		RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKAKIE	
msa277662.2{330_M781}		RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKAKIE	
msa277662.2{330_JM9130013}		RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKAKIE	
msa277662.2{330_090}		RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGn	GHVKLFKAKIE	
msa277662.2{330_2603}		RDNADIRFGL	EQGLNFIAIS	FVRTAKDVNE	VRAICEETGx	GHVKLFKAKIE	
Consensus		*****	*****	*****	*****	*****	

Table 72: Comparative Sequences relating to SAG0941

	251				300
msa277662.2{330_18RS21}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_A909}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_CJB110}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_H36B}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_1169NT}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_COH1}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_M732}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_M781}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_JM9130013}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_090}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
msa277662.2{330_2603}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM	IITKVNAAGK
Consensus	*****	*****	*****	*****	*****
	301				350
msa277662.2{330_18RS21}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_A909}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_CJB110}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_H36B}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_1169NT}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_COH1}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_M732}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_M781}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_JM9130013}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_090}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_2603}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
Consensus	*****	*****	*****	*****	*****
	351				400
msa277662.2{330_18RS21}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAAS	VKDATHSMDI
msa277662.2{330_A909}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAAS	VKDATHSMDI
msa277662.2{330_CJB110}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAAS	VKDATHSMDI
msa277662.2{330_H36B}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAAS	VKDATHSMDI
msa277662.2{330_1169NT}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAAS	VKDATHSMDI
msa277662.2{330_COH1}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAAS	VKDATHSMDI
msa277662.2{330_M732}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAAS	VKDATHSMDI
msa277662.2{330_M781}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAAS	VKDATHSMDI
msa277662.2{330_JM9130013}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAAS	VKDATHSMDI
msa277662.2{330_090}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAAS	VKDATHSMDI
msa277662.2{330_2603}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAAS	VKDATHSMDI
Consensus	*****	*****	*****	*****	*****
	401				450
msa277662.2{330_18RS21}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_A909}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_CJB110}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_H36B}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_1169NT}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_COH1}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_M732}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_M781}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_JM9130013}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_090}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
msa277662.2{330_2603}	KLVTITETG	NTARAIKFR	PDADILAVTF	DEKVQSLMI	NWGVIPVLAD
Consensus	*****	*****	*****	*****	*****
	451				500
msa277662.2{330_18RS21}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_A909}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_CJB110}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_H36B}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_1169NT}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_COH1}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_M732}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_M781}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_JM9130013}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_090}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
msa277662.2{330_2603}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNTMRVRTVK
Consensus	*****	*****	*****	*****	*****

Table 73: Comparative Sequences relating to SAG0981

SEQ ID NO. 7301

STRAIN 2603

TTGCTCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTATTTAGCATTAAATCGGTGAT
 ATCATTAAATCAAACAGATACCTGAAACGTGAAACCTTCCAAACAGTCTTTTCAGCAACTA
 ATGACCGAACTATCTGATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCT
 GGTGATGAATTTCAAGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGACCAT
 ATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGCCCTCGGTACAGGAAACATTATA
 ACATCCATCAATTCAAATGAAAGTATCGGTGCTGATGGTCTGCCTACTGGCATGCTCGC
 TCAGCTATTAAATCATATACATGATAAAATGATTATGGAACAGTTCAAGTAGCTATTGTC
 CTTGATGATGAAGACCAAAACCTTGAATTAACACTAAATAGTCTCATTTACAGCTGGTGAT
 TTTATCAAGTCAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAA
 GATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGGAAAATATTGAACCT
 AGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCTGAAGATTACTTAAGAACGAGAACA
 CAGGCAGCCGATCTATTAGTTAAAGTTGCACCTCAAACTAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7302

STRAIN 090

TCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTATTT
 AGCATTAAATCGGTGATATCATTAAATCAAACAGATACCTGAAACGTGAAA
 CTTTCCAAACAGTCTTTTCAGCAAACTAATGACCGAACTATCTGATGTATAT
 GGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGATGAATTTCA
 AGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGACCATATTTC
 AACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGCCCTCGGTACAGGAAAC
 ATTATAACATCCATCAATTTAAATGAAAGTATCGGTGCTGATGGTCTGCTG
 CTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAAAATGATT
 ATGGAACAGTTTCAAGTAGCTATTGCTTGGATGATGAAGACCAAAACCTT
 GAATTAACACTAAATAGTCTCATTTACAGCTGGTGATTTTATCAAGTCAAA
 ATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAAGATA
 ATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGGAAAATATT
 GAACCTAGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCTGAAGATTTA
 CTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAGTTGCACCTC
 AAATAAGGGGAAGCTATGATTTC

SEQ ID NO. 7303

STRAIN A909

TCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTAT
 TTAGCATTAAATCGGTGATATCATTAAATCAAACAGATACCTGAAACGTGA
 AACTTTCCAAACAGTCTTTTCAGCAACTAATGACCGAACTATCTGATGTAT
 ATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGATGAATTT
 CAAGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGACCATAT
 TCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGCCCTCGGTACAGGAA
 ACATTATAACATCCATCAATTTCAAATGAAAGTATCGGTGCTGATGGTCTCT
 GCCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAAAATGA
 TTATGGAACAGTTCAAGTAGCTATTGCTTGGATGATGAAGACCAAAACC
 TTGAATTAAACACTAAATAGTCTCATTTACAGCTGGTGATTTTATCAAGTCA
 AAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAAGA
 TAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGGAAAATA
 TTGAACCTAGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCTGAAGATT
 TACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAGTTGCAC
 TCAAACTAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7304

STRAIN H36B

TCTGCTATAATAGACAAAAAGGTGGTGATATTT
 ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAACAGATACCTTGA
 ACGTGAACCTTTCCAAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG
 ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
 GAATTTCAAGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGA
 CCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGCCCTCGGTA
 CAGGAACATTATAACATCCATCAATTTCAAATGAAAGTATCGGTGCTGAT
 GGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAA
 AAATGATTATGGAACAGTTCAAGTAGCTATTGCTTGGATGATGAAGACC
 AAAACCTTGAATTAAACACTAAATAGTCTCATTTACAGCTGGTGATTTTATC
 AAGTCAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
 TCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCTG
 AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACTAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7305

STRAIN 18RS21

TCTGCTATAATAGACAAAAAGGTGGTGATATTT
 ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAACAGATACCTTGA
 ACGTGAACCTTTCCAAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG
 ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
 GAATTTCAAGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGA
 CCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGCCCTCGGTA
 CAGGAACATTATAACATCCATCAATTTCAAATGAAAGTATCGGTGCTGAT
 GGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAA
 AAATGATTATGGAACAGTTCAAGTAGCTATTGCTTGGATGATGAAGACC
 AAAACCTTGAATTAAACACTAAATAGTCTCATTTACAGCTGGTGATTTTATC
 AAGTCAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
 TCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAAGCAAGCGGTCTG
 AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACTAAAGGGGAAGCTATGATTTC

Table 73: Comparative Sequences relating to SAG0981

TCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAGCAAGCGGTCTG
 AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACATAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7306

STRAIN M732

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 TATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTG
 AACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCT
 GATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
 TGAATTTCAAGCTTTATTTGAACaATCAAAAAAGGTATTTCAAATTTATTG
 ACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGT
 ACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGA
 TGGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATA
 AAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGAC
 CAAAACCTTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTAT
 CAAGTCAAAATGGACTACAAACCAATTTCAAATGCTTGAGCACTTAATAC
 TTCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTG
 GAAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAGCAAGCGGTCT
 GAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 GTTGCACTCAAACATAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7307

STRAIN COH1

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 TATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTG
 AACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCT
 GATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
 TGAATTTCAAGCTTTATTTGAACaATCAAAAAAGGTATTTCAAATTTATTG
 ACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGT
 ACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGA
 TGGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATA
 AAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGAC
 CAAAACCTTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTAT
 CAAGTCAAAATGGACTACAAACCAATTTCAAATGCTTGAGCACTTAATAC
 TTCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTG
 GAAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAGCAAGCGGTCT
 GAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 GTTGCACTCAAACATAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7308

STRAIN M781

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTGA
 ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG
 ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
 GAATTTCAAGCTTTATTTGAACAAATCAAAAAAGGTATTTCAAATTTATTGA
 CCAATTTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCGGTGA
 CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
 GGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAA
 AATGATTATGGAACAGTTCAAGTAGCTATTTGCCITGATGATGAAGACC
 AAAACCTTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTATC
 AAGTCAAAATGGACTACAAACCAATTTCAAATGCTTGAGCACTTAATACT
 TCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAGCAAGCGGTCTG
 AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACATAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7309

STRAIN CJB110

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 TTTATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACT
 TGAACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTAT
 CTGATGTATATGGTGAAGAGCTGATTTCTCTATTCACTATTACAGCTGGT
 GATGAATTTCAAGCTTTATTTGAACCAATCAAAAAAGGTATTTCAAATTTAT
 TGACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTTCGGCCTCG
 GTACAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCT
 GATGGTCTGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATA
 TAAAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCITGATGATGAAG
 ACCAAAACCTTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTT
 ATCAAGTCAAAATGGACTACTAACCATTTCAAATGCTTGAGCACTTAAT
 ACTTCAAGATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCACT
 TGAAAAATATTGAACCTAGTGCCTGACTAAACGCCCTTAAGCAAGCGGT
 CTGAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAA
 AAGTTGCACTCAAACATAAGGGGGAAGCTATGATTTC

SEQ ID NO. 7310

STRAIN JM9130013

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAAACAGATACTTGA
 ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG

Table 73: Comparative Sequences relating to SAG0981

ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT GAATTTCAAGCTTTATGAAACCATCAAAAAAGGTATTTCAAATTATTGA CCATATTCAACTAGCTCTAAACCTGTTAATGTAAGGTTCCGGCTCGGTA CAGGAAACATTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT GGTCTGCTACTGCGCATGCTCGCTCAGCTATTATCATATACATGATAA AAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACC AAAACCTTGAATTAACTAACTAAATAGTCTCATTTCAGCTGGTGATTTTATC AAGTCAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT TCAAGATAATTATCAAGAACAATTTCAACATCAAAAGTTAGCCCACTGG AAAAATATTGAACCTAGTGGCTGACTAAACGCCTTAAGCAAGCGGTCTG AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG TTGCACTCAAATAAAGGGGAAGCTATGATTTTC					
PRETTY of: /biotmp/msa31912.2{*} February 18, 2003 08:19 ..					
msa31912.2{338_18RS21}	1	50			
msa31912.2{338_2603}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_A909}	ttgTCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_H36B}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_JM9130013}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_COH1}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_M732}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_M781}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_090}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	aTATTTATGT	ATTAGCATT
msa31912.2{338_CJB110}	---TCTGCTA	TAATAGACAA	AAAGGTGGTG	gTATTTATGT	ATTAGCATT
Consensus	*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	51	100			
msa31912.2{338_2603}	AATCGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_A909}	AATCGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_H36B}	AATCGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_JM9130013}	AATCGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_COH1}	AATCGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_M732}	AATCGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_M781}	AATCGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_090}	AATCGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
msa31912.2{338_CJB110}	AATCGGTGAT	ATCATTAAAT	CAAAACAGAT	ACTTGAACGT	GAAACTTTCC
Consensus	*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	101	150			
msa31912.2{338_2603}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_A909}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_H36B}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_JM9130013}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_COH1}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_M732}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_M781}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_090}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
msa31912.2{338_CJB110}	AACAGTCTTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT	ATATGGTGAA
Consensus	*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	151	200			
msa31912.2{338_2603}	GAGCTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_A909}	GAGCTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_H36B}	GAGCTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_JM9130013}	GAGCTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_COH1}	GAGCTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_M732}	GAGCTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_M781}	GAGCTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_090}	GAGCTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
msa31912.2{338_CJB110}	GAGCTGATTT	CTCATTAC	TATTACAGCT	GGTGATGAAT	TTCAAGCTTT
Consensus	*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	201	250			
msa31912.2{338_2603}	ATTGAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_A909}	ATTGAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_H36B}	ATTGAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_JM9130013}	ATTGAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_COH1}	ATTGAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_M732}	ATTGAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_M781}	ATTGAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_090}	ATTGAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
msa31912.2{338_CJB110}	ATTGAAACCa	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT	ATTCAACTAG
Consensus	*****-*	*****	*****	*****	*****
msa31912.2{338_18RS21}	251	300			
msa31912.2{338_2603}	CTCTAAACCC	TGTTAATGTA	AGGTTCCGCC	TCGGTACAGG	AAACATTATA
	CTCTAAACCC	TGTTAATGTA	AGGTTCCGCC	TCGGTACAGG	AAACATTATA

Table 73: Comparative Sequences relating to SAG0981

msa31912.2{338_A909}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
msa31912.2{338_H36B}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
msa31912.2{338_JM9130013}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
msa31912.2{338_COH1}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
msa31912.2{338_M732}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
msa31912.2{338_M781}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
msa31912.2{338_090}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
msa31912.2{338_CJB110}	CTCTAAAACC	TGTTAATGTA	AGGTTTCGGCC	TCGGTACAGG	AAACATTATA		
Consensus	*****	*****	*****	*****	*****		
msa31912.2{338_18RS21}	301	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	350	CTGCCTACTG
msa31912.2{338_2603}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_A909}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_H36B}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_JM9130013}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_COH1}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_M732}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_M781}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_090}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
msa31912.2{338_CJB110}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG		
Consensus	*****	***_*****	*****	*****	*****		
msa31912.2{338_18RS21}	351	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	400	GATTATGGAA
msa31912.2{338_2603}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_A909}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_H36B}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_JM9130013}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_COH1}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_M732}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_M781}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_090}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
msa31912.2{338_CJB110}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA		
Consensus	*****	*****	*****	*****	*****		
msa31912.2{338_18RS21}	401	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	450	CCTTGAATTA
msa31912.2{338_2603}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_A909}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_H36B}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_JM9130013}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_COH1}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_M732}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_M781}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_090}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
msa31912.2{338_CJB110}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA		
Consensus	*****	*****	*****	*****	*****		
msa31912.2{338_18RS21}	451	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	500	CAAAATGGAC
msa31912.2{338_2603}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_A909}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_H36B}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_JM9130013}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_COH1}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_M732}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_M781}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_090}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
msa31912.2{338_CJB110}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC		
Consensus	*****	*****	*****	*****	*****		
msa31912.2{338_18RS21}	501	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	550	GATAAATTATC
msa31912.2{338_2603}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_A909}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_H36B}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_JM9130013}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_COH1}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_M732}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_M781}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_090}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
msa31912.2{338_CJB110}	TACaAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAAATTATC		
Consensus	***_*****	*****	*****	*****	*****		
msa31912.2{338_18RS21}	551	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AAGTTAGCCC	600	TATTGAACCT
msa31912.2{338_2603}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AAGTTAGCCC	TATTGAACCT		
msa31912.2{338_A909}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AAGTTAGCCC	TATTGAACCT		
msa31912.2{338_H36B}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AAGTTAGCCC	TATTGAACCT		
msa31912.2{338_JM9130013}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AAGTTAGCCC	TATTGAACCT		
msa31912.2{338_COH1}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AAGTTAGCCC	TATTGAACCT		
msa31912.2{338_M732}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AAGTTAGCCC	TATTGAACCT		

Table 73: Comparative Sequences relating to SAG0981

msa31912.2{338_M781}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_090}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_CJB110}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
Consensus	*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_2603}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_A909}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_H36B}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_JM9130013}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_COH1}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_M732}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_M781}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_090}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_CJB110}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
Consensus	*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_2603}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_A909}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_H36B}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_JM9130013}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_COH1}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_M732}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_M781}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_090}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_CJB110}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
Consensus	*****	*****	*****	*****	*****
msa31912.2{338_18RS21}	AAGGGGAAG	CTATGATTTC			
msa31912.2{338_2603}	AAGGGGAAG	CTATGATTTC			
msa31912.2{338_A909}	AAGGGGAAG	CTATGATTTC			
msa31912.2{338_H36B}	AAGGGGAAG	CTATGATTTC			
msa31912.2{338_JM9130013}	AAGGGGAAG	CTATGATTTC			
msa31912.2{338_COH1}	AAGGGGAAG	CTATGATTTC			
msa31912.2{338_M732}	AAGGGGAAG	CTATGATTTC			
msa31912.2{338_M781}	AAGGGGAAG	CTATGATTTC			
msa31912.2{338_090}	AAGGGGAAG	CTATGATTTC			
msa31912.2{338_CJB110}	AAGGGGAAG	CTATGATTTC			
Consensus	*****	*****			

SEQ ID NO. 7311

STRAIN 2603 frame: 1

LSAIDKKVVFMYLALIGDIINSKQILERETFQOSFQQLMTELSDVYGEELISPFTTITA
 DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHAR
 SAINHIHDKNDYGTQVVAICLDDQNLLETLNLSISAGDFIKSKWTTNHFQMLEHLILQ
 DNYQEQFQHQLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCQTQTKGGSYDF

SEQ ID NO. 7312

STRAIN 090 frame: 1

SAIDKKVVFMYLALIGDIINSKQILERETFQOSFQQLMTELSDVYGEELISPFTTITAG
 DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINLNSIGADGPAYWHARS
 AINHIHDKNDYGTQVVAICLDDQNLLETLNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQFQHQLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCQTQTKGGSYDF

SEQ ID NO. 7313

STRAIN A909 frame: 1

SAIDKKVVFMYLALIGDIINSKQILERETFQOSFQQLMTELSDVYGEELISPFTTITAG
 DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVVAICLDDQNLLETLNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQFQHQLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCQTQTKGGSYDF

SEQ ID NO. 7314

STRAIN H36B frame: 1

SAIDKKVVFMYLALIGDIINSKQILERETFQOSFQQLMTELSDVYGEELISPFTTITAG
 DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVVAICLDDQNLLETLNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQFQHQLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCQTQTKGGSYDF

SEQ ID NO. 7315

STRAIN 18RS21 frame: 1

SAIDKKVVFMYLALIGDIINSKQILERETFQOSFQQLMTELSDVYGEELISPFTTITAG
 DEFQALLKPSKKVFQIIDHIQLALKPVNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVVAICLDDQNLLETLNLSISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEQFQHQLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCQTQTKGGSYDF

SEQ ID NO. 7316

STRAIN M732 frame: 1

SAIDKKVVFMYLALIGDIINSKQILERETFQOSFQQLMTELSDVYGEELISPFTTITAG

Table 73: Comparative Sequences relating to SAG0981

DEFQALLKQSKKVFQIIDHIQLALKPNNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTGVQVAICLDDDEDQNLLELTNLSISAGDFIKSKWTNNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENI EPSALT KRLKASGLKIYLRTRTQAADLLVKSCQTQTGGGSYDF

SEQ ID NO. 7317

STRAIN COH1 frame: 1

SAIIDKKVVFMYLALIGDI INSKQILERET FQQSFQQLMTELSDVYGEELISPFTITAG
 DEFQALLKQSKKVFQIIDHIQLALKPNNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTGVQVAICLDDDEDQNLLELTNLSISAGDFIKSKWTNNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENI EPSALT KRLKASGLKIYLRTRTQAADLLVKSCQTQTGGGSYDF

SEQ ID NO. 7318

STRAIN M781 frame: 1

SAIIDKKVVFMYLALIGDI INSKQILERET FQQSFQQLMTELSDVYGEELISPFTITAG
 DEFQALLKQSKKVFQIIDHIQLALKPNNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTGVQVAICLDDDEDQNLLELTNLSISAGDFIKSKWTNNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENI EPSALT KRLKASGLKIYLRTRTQAADLLVKSCQTQTGGGSYDF

SEQ ID NO. 7319

STRAIN CJB110 frame: 1

SAIIDKKVVFMYLALIGDI INSKQILERET FQQSFQQLMTELSDVYGEELISLFTITAG
 DEFQALLKQSKKVFQIIDHIQLALKPNNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTGVQVAICLDDDEDQNLLELTNLSISAGDFIKSKWTNNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENI EPSALT KRLKASGLKIYLRTRTQAADLLVKSCQTQTGGGSYDF

SEQ ID NO. 7320

STRAIN JM9130013 frame: 1

SAIIDKKVVFMYLALIGDI INSKQILERET FQQSFQQLMTELSDVYGEELISPFTITAG
 DEFQALLKQSKKVFQIIDHIQLALKPNNVRFGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTGVQVAICLDDDEDQNLLELTNLSISAGDFIKSKWTNNHFQMLEHLILQD
 NYQEQQFQHQKLAQLENI EPSALT KRLKASGLKIYLRTRTQAADLLVKSCQTQTGGGSYDF

PRETTY of: /biotmp/msa32053.2{*} February 18, 2003 08:25 ..

	1		50
msa32053.2{338_18RS21}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_2603}	1SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_A909}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_CJB110}	~SAIIDKKVV	vFMYLALIGD	I INSKQILER
msa32053.2{338_COH1}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_H36B}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_JM9130013}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_M732}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_M781}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
msa32053.2{338_090}	~SAIIDKKVV	iFMYLALIGD	I INSKQILER
Consensus	*****	-*****	*****

	51		100
msa32053.2{338_18RS21}	ELISpFTITA	GDEFQALLKp	SKKVFQIIDH
msa32053.2{338_2603}	ELISpFTITA	GDEFQALLKp	SKKVFQIIDH
msa32053.2{338_A909}	ELISpFTITA	GDEFQALLKp	SKKVFQIIDH
msa32053.2{338_CJB110}	ELISpFTITA	GDEFQALLKp	SKKVFQIIDH
msa32053.2{338_COH1}	ELISpFTITA	GDEFQALLKq	SKKVFQIIDH
msa32053.2{338_H36B}	ELISpFTITA	GDEFQALLKp	SKKVFQIIDH
msa32053.2{338_JM9130013}	ELISpFTITA	GDEFQALLKp	SKKVFQIIDH
msa32053.2{338_M732}	ELISpFTITA	GDEFQALLKq	SKKVFQIIDH
msa32053.2{338_M781}	ELISpFTITA	GDEFQALLKq	SKKVFQIIDH
msa32053.2{338_090}	ELISpFTITA	GDEFQALLKp	SKKVFQIIDH
Consensus	****-****	*****	*****

	101		150
msa32053.2{338_18RS21}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_2603}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_A909}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_CJB110}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_COH1}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_H36B}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_JM9130013}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_M732}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_M781}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
msa32053.2{338_090}	TSINsNESIG	ADGPAYWHAR	SAINHIHDKN
Consensus	****-****	*****	*****

	151		200
msa32053.2{338_18RS21}	TLNSLSISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_2603}	TLNSLSISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_A909}	TLNSLSISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_CJB110}	TLNSLSISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_COH1}	TLNSLSISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_H36B}	TLNSLSISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_JM9130013}	TLNSLSISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_M732}	TLNSLSISAGD	FIKSKWTTNH	FQMLEHLILQ
msa32053.2{338_M781}	TLNSLSISAGD	FIKSKWTTNH	FQMLEHLILQ
Consensus	TLNSLSISAGD	FIKSKWTTNH	FQMLEHLILQ

Table 73: Comparative Sequences relating to SAG0981

msa32053.2{338_090}	TLNSLISAGD	FIKSKWTTNH	FQMLEHLILQ	DNYQEQFQHQ	KLAQLENIEP
Consensus	*****	*****	*****	*****	*****
	201			240	
msa32053.2{338_18RS21}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_2603}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_A909}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_CJB110}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_COH1}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_H36B}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_JM9130013}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_M732}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_M781}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_090}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
Consensus	*****	*****	*****	*****	

Table 74: Comparative Sequences relating to SAG1572

SEQ ID NO. 7401

STRAIN 2603

ATGGAAATGCAAGTTCAAAAAGTTTAAATCAAATATACATTACGGAACACTCTAT
CTAGTCCCACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCATTAGGATTTTA
AGAGAAGTTGATTTTATTTGTGCAGAGGATACACGAAATACGGGACTTTTACTCAAGCAC
TTTGATATTACTACTAAACAAATTAGTTTTCACGAAACAAATGCTTACGATAAAATCTCT
GGGTTAATTGATTTGTTAAAGAAGGGAATCTTTAGCCCAAGTATCTGATGCAGGAATG
CCCTCTATTTCGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCA
GTTGTATCTATACCAAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTCAGGTTTAGCT
CCACAACCTCATATTTTATGGCTTCTTACCTCGTAAGAAAGGTCAACAAATAACTTTC
TTTGAACAAAGCAAGATTACCTGAAACACAAATCTTTATGAGTCACCGTTTCGAGTC
TCTGATACGCTAAACACATGAAAGAGATTTCGGGAGATCGCCAAGTTGTTTATGACGC
GAATTGACGAACTCTATGAAGAGTATCAAAGAGGAACCAATTAGTCAACTTTTAGAGCAT
ATTGAAAGGTTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGGTAAAGAGATACCG
GAGCGAGTGAAGACAGTAGCCAACAAGATCCACTAGTATTAGTAAAGAATATATCGCT
AATGGTGATAAACTAATCAAGCGATAAAAAAGTAGCAAGAATTTAATCTCAATAGA
CAAGAACTCTATGCTAGTTTCCATGATTTA

SEQ ID NO. 7402

STRAIN 090

GAAATGCAAGTTCAAAAAGTTTAAATCAAATACACATTACGGGACACT
CTATCTAGTCCCACTCCAATTGGTAATCTAGATGATATGACTTTTCGTG
CCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGGATACACGA
AATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTAG
TTTTACGAAACAAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGT
TAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCT
ATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGGGAT
CCCGTCTGATCTATACCAAGGAGCTAGCGCTGGTATTACTGCTCTCATCG
CTTCAGGTTTAGCTCCACAACCTCATATTTTATGGCTTCTTACCGCGT
AAGAAAGGTCAACAAATACTTTTGTAAACAAAGAAAGATTACCCCTGA
AACCAAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTAAAC
ACATGAAGAGATTACCGGAGATCGCCAAGTTGTTTATGACGGAATTG
ACGAACTCTATGAAGAGTATCAAAGAGGAACCAATTAGTCAACTTTTAGG
GCATATTGAAAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATG
GTAAGAGAGATACCGAGCGAGTGAAGACAGTAGCCAACAAGATCCACTA
GTATTAGTAA

SEQ ID NO. 7403

STRAIN A909

AGTTCAAAAAAGTTTAAATCAAATATACATTACGGAACACTCTATCTAG
TCCCACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCATTAGG
ATTTAAGAGAAGTTGATTTTATTTGTGCAGAGGATACACGAAATACGGG
ACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTAGTTTTCAGC
AACAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGTTAAAGAA
GGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCTATTCTGA
CCCGAGCATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCAAGTTG
TATCTATACCAAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTCAGG
TTAGCTCCACAACCTCATATTTTATGGCTTCTTACCACGTAAGAAAGG
TCAACAAATAACTTTCTTTGAACAAAGCAAGATTACCCCTGAAACACAAA
TCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTAAACACATGAAA
GAGATTACCGGAGATCGCCAAGTTGTTTATGACGGAATTGACGAAACT
CTATGAAGAGTATCAAAGAGGAACCAATTAGTCAACTTTTAGAGCATATTG
AAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGGTAAAGAGA
GATACCGAGCGAGTGAAGACAGTAGCCAACAAGATCCACTAGTATTAGT
AA

SEQ ID NO. 7404

STRAIN H36B

GAAATGCAAGTTCAAAAAGTTTAAATCAAATACACATT
ACGGGACACTCTATCTAGTCCCACTCCAATTGGTAATCTAGATGATATG
ACTTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGA
GGATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTA
AACAAATTAGTTTTCACGAACACAATGCTTATGATAAAATCTCTGGGTTA
ATTGATTGTTAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGG
AATGCCCTCTATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTG
AAGGGGATATCCCGTCTATCTATACCAAGGAGCTAGCGCTGGTATTACT
GCTCTCATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTATGGCTT
CTTACCGGTAAAGCAAGGTCAACAAATAACTTTTGTAAACAAAGAAAG
ATTACCCCTGAAACACAAATCTTTATGAGTCACCGTTTCGAGTCTCTGAT
ACGCTAAACACATGAAAGAGATTATGGAGATCGCCAAGTTGTTTATGAT
ACCGAATTGACGAACTCTATGAAGAGTATCAAAGAGGAACCAATTAGTCA
AACTTTTAGGGCATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATT
ATTGTTGATGGTAAAGAGATACCTGAGCGAGTGAAGACAGTAGCCAACA
AGATCCACTAGTATTAGTAA

SEQ ID NO. 7405

STRAIN 18RS21

GAAATGCAAGTTCAAAAAGTTTAAATCAAATATACATT
ACGGAACACTCTATCTAGTCCCACTCCAATTGGTAATCTAGATGATATG
ACTTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGA
GGATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTA
AACAAATTAGTTTTCACGAACACAATGCTTACGATAAAATCTCTGGGTTA
ATTGATTGTTAAAGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGG

Table 74: Comparative Sequences relating to SAG1572

AATGCCCTCTATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTG
AAGGGGATATCCAGTTGTATCTATACCAGGAGCTAGCGCTGGTATTACT
GCTCTCATCGCTTCAGTTTGTCTCCACACCTCATATTTTTATGGCTT
CTTACCACGTAAGAAAGGTCAACAAATAACTTTCTTTGAAACAAAGCAAG
ATTACCCCTGAAACACAAATCTTTATGAGTCACCGTTTCGAGTCTCTGAT
ACGCTAAACACATGAAAGAGATTACGGAGATCGCCAAGTTGTTTAGT
ACGCCAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTC
AACTTTTAGAGCATATTGAAAGGTCCCTCTCAAAGGTGAATGCTTAATT
ATTGTTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACA
AGATCCACTAGTATTAGTAA

SEQ ID NO. 7406

STRAIN M732

GAAATGCAAGTTCAAAAAAGTTTAAATCAAAT
ATACATTACGGAACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGA
TGATATGACTTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTT
GTGAGAGGATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATT
ACTACTAAACAAATTAGTTTTCACGAACCAATGCTTACGATAAAATCTC
TGGGTTAATTGATTTGTAAAGAAGGGAATCTTTAGCCCAAGTATCTG
ATGACGGAATGCCCTCTATTCTGACCCAGGACATGACCTTGTCAAGGCT
GCTATTGAAGGGGATATCCAGTTGTATCTATACCAGGAGCTAGCGCTGG
TATTACTGCTCTCATCGCTTCAGTTTAGCTCCCAACCTCATATTTTTT
ATGGCTTCTTACCACGTAAGAAAGGTCAACAAATAACTTTCTTTGAAACA
AAGCAAGATTACCTGAAACACAAATCTTTTATGAGTCACCGTTTCGAGT
CTCTGATACGCTAAACACATGAAAGAGATTACGGAGATCGCCAAGTTG
TTTTAGTACGCGAATTGACGAACTCTATGAAGAGTATCAAAGAGGAACC
ATTAGTCAACTTTTAGAGCATATTGAAAGGTCCCTCTCAAAGGTGAATG
CTTAATTATGTTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTA
GCCAACAAGATCCACTAGTATTAGTAA

SEQ ID NO. 7407

STRAIN COH1

GAAATGCAAGTTCAAAAAAGTTTAAATCAAATATACATTAC
GGAACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGAC
TTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGAGAGG
ATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAA
CAAAATAGTTTTCACGAACCAATGCTTACGATAAAATCTCTGGGTTAAT
TGATTTGTAAAGAAGGGAATCTTTAGCCCAAGTATCTGATGACAGGAA
TGCCCTCTATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAA
GGGATATCCAGTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCT
TCTCATCGCTTCAGGTTTAGCTCCCAACCTCATATTTTTATGGCTTCT
TACCAGTTAAGAAAGGTCAACAAATAACTTTCTTTGAAACAAAGCAAGAT
TACCTGAAACACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATAC
GCTAAACACATGAAAGAGATTACGGAGATCGCCAAGTTGTTTATGATAC
GCGAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAA
CTTTTAGAGCATATTGAAAGGTCCCTCTCAAAGGTGAATGCTTAATTAT
TGTTGATGGTAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAG
ATCCACTAGTATTAGTAA

SEQ ID NO. 7408

STRAIN M781

AAATGCAAGTTCAAAAAAGTTTAAATCAAATATACATTACGGAACACTC
TATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGC
CATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGACAGGATACACGAA
ATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTAGT
TTTCACGAACCAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGTT
AAAAAGAGGGAATCTTTAGCCCAAGTATCTGATGACGGAATGCCCTCTA
TTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATC
CCAGTTGTATCTATACAGGAGCTAGCGCTGGTATTACTGCTCTCATCGC
TTCAGGTTTAGCTCCCAACCTCATATTTTTTATGGCTTCTTACCAGTA
AGAAAGGTCAACAAATAACTTTCTTTGAAACAAAGCAAGATTACCTGAA
ACACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTAAACCA
CATGAAAGAGATTACGGAGATCGCCAAGTTGTTTATGATACGGAATTGA
CGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAGAG
CATATTGAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGG
TAAGAGAGATACCGAGCGAGTGAAAGACAGTAGCCAACAAGATCCACTAG
TATTAGTAA

A

SEQ ID NO. 7409

STRAIN CJB110

GAAATGCAAGTTCAAAAAAGTTTAAATCAAATACATTACGGGACAC
TCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTTCGT
GCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGACAGGATACACG
AAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAAATTA
GTTTTACGAACCAATGCTTACGATAAAATCTCTGGGTTAATTGATTTG
TTAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGACGGAATGCCCTC
TATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGGGA
TCCCGGTGCTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATC
GCTTCAGGTTTAGCTCCCAACCTCATATTTTTTATGGCTTCTTACCAGG
TAAGAAAGGTCAACAAATAACTTTCTTTGAAACAAAGAAAGATTACCTG
AAACCAAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTAAAC
CATGAAAGAGATTACGGAGATCGCCAAGTTGTTTATGATACGCGAATT

Table 74: Comparative Sequences relating to SAG1572

GACGAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAG
GGCATATTGAAAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGAT
GGTAAGAGAGATACCGAGCGAGTGAAGACAGTAGCCAACAGATCCACT
AGTATTAGTAA

SEQ ID NO. 7410

STRAIN 1169NT

TGCAAGTTCAAAAAAGTTTAAATCAAATACACATTATGGGACACTCTAT
CTAGTCCCAACTCCAATTGGTAATCTAGATGATGACTTTTCGTGCCAT
TAGGATTTTAAGAGAGTTGaTTTATTGTGTCAGAGGATACAGAAATA
CGGCACITTTACTCAAGCAGCTTTGATaTTACTACTAAACAAATTAGTtTTT
cACGAACACAATGCTTACGATAAAATCTCTGGGTTAATTGATTtGTTAAA
AGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCTATT
CTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCA
GTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTC
AGGTTTAGCTCCACAACCTCATATTTTATGGCTTCTTACCACGTAAGA
AAGGTCAACAATAACTTTTGTGAAACAAGCAAGATTATCTGAAACA
CAAATCTTTTATGAGTCAACCGtTTGAGTCTCTGATACGCTAAACACAT
GAAAGAGATTTACGGAGATCGCCAAGTTGTTTATGACGCAATTGACgA
AACTCTATGAAGAGTATCAAAGAGGAACCATTaGTCAACTTTTAGAGCAT
ATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGtTGATGGTAA
GAGAGATaCCGAGCGAGTGAAGACAGTAGCCAACAAGATCCACTAGTAT
TAGTAA

SEQ ID NO. 7411

STRAIN JM9130013

GAAATGCAAGTTCAAAAAAGTTTAAATCAAATACACATTACGGGA
CACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATGACTTTT
CGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTGTGTCAGAGGATAC
ACGAAATACGGGACTTTTACTCAAGCAGCTTTGATATTACTACTAAACAA
TTAGTTTTCACGAACACAATGCTTATGATAAAATCTCTGGGTTAATTGAT
TTGTTAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCC
CTCTATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGG
ATATCCCGGTGCTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTC
ATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTATGGCTTCTTACC
GCGTAAGCAAGGTCAACAAATAACtTTTTTGAACAAGAAAGATTACC
CTGAAACACAATCTTTTATGAGTCAACCGTTTCGAGTCTCTGATACGCTA
AAACACATGAAGAGATTTATGGAGATCGCCAAGTTGTTTATGACGCGA
ATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCACTTT
TAGGGCATATTGaaaAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTT
GATGGTAAGAGAGATACTAGCGAGTGAAGACAGTAGCCAACAAGATCC
AGTAGTATTAGTAA

PRETTY of: /biotmp/msa323014.2{*} March 28, 2003 02:40 ..

	1		50
msa323014.2{343_18RS21}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_A909}	-----	-AGTTCAAAA	AAGTTTTAAA
msa323014.2{343_COH1}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_M732}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_M781}	---aaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_2603}	atggaaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_1169NT}	-----	atggaaatgc	aAGTTCAAAA
msa323014.2{343_090}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_CJB110}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_H36B}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA
msa323014.2{343_JM9130013}	---gaaatgc	aAGTTCAAAA	AAGTTTTAAA
Consensus	*****	*****	*****

	51		100
msa323014.2{343_18RS21}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_A909}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_COH1}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_M732}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_M781}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_2603}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_1169NT}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_090}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_CJB110}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_H36B}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
msa323014.2{343_JM9130013}	ACTCTATCTA	GTCCCAACTC	CAATTGGTAA
Consensus	*****	*****	*****

	101		150
msa323014.2{343_18RS21}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT
msa323014.2{343_A909}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT
msa323014.2{343_COH1}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT
msa323014.2{343_M732}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT
msa323014.2{343_M781}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT
msa323014.2{343_2603}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT
msa323014.2{343_1169NT}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT
msa323014.2{343_090}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT

Table 74: Comparative Sequences relating to SAG1572

msa323014.2{343_CJB110}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT	TTATTGTGTC	AGAGGATACA
msa323014.2{343_H36B}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT	TTATTGTGTC	AGAGGATACA
msa323014.2{343_JM9130013}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT	TTATTGTGTC	AGAGGATACA
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_A909}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_COH1}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_M732}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_M781}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_2603}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_1169NT}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_090}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_CJB110}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_H36B}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_JM9130013}	CGAAATACGG	GACTTTTACT	CAAGCACITTT	GATATTACTA	CTAAACAAAT
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_A909}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_COH1}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_M732}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_M781}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_2603}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_1169NT}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_090}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_CJB110}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_H36B}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_JM9130013}	TAGTTTTCAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
Consensus	*****	*****	****-*****	*****	*****
msa323014.2{343_18RS21}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_A909}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_COH1}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_M732}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_M781}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_2603}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_1169NT}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_090}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_CJB110}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_H36B}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
msa323014.2{343_JM9130013}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCCC
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_A909}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_COH1}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_M732}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_M781}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_2603}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_1169NT}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_090}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_CJB110}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_H36B}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_JM9130013}	TCTATTTCCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	tATCCCaGtT	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_A909}	tATCCCaGtT	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_COH1}	tATCCCaGtT	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_M732}	tATCCCaGtT	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_M781}	tATCCCaGtT	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_2603}	tATCCCaGtT	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_1169NT}	tATCCCaGtT	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_090}	gATCCCGtTc	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_CJB110}	gATCCCGtTc	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_H36B}	tATCCCGtTc	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_JM9130013}	tATCCCGtTc	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
Consensus	-*****-	*****	*****	*****	*****
msa323014.2{343_18RS21}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_A909}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_COH1}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_M732}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_M781}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_2603}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_1169NT}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa

Table 74: Comparative Sequences relating to SAG1572

msa323014.2{343_090}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCg	
msa323014.2{343_CJB110}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCg	
msa323014.2{343_H36B}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCg	
msa323014.2{343_JM9130013}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCg	
Consensus	*****	*****	*****	*****	*****	
msa323014.2{343_18RS21}	451	CGTAAGaAAG	GTCAACAAAT	AACITTTcTTT	GAAACAAAGc	AAGATTAcCC
msa323014.2{343_A909}	CGTAAGaAAG	GTCAACAAAT	AACITTTcTTT	GAAACAAAGc	AAGATTAcCC	
msa323014.2{343_COH1}	CGTAAGaAAG	GTCAACAAAT	AACITTTcTTT	GAAACAAAGc	AAGATTAcCC	
msa323014.2{343_M732}	CGTAAGaAAG	GTCAACAAAT	AACITTTcTTT	GAAACAAAGc	AAGATTAcCC	
msa323014.2{343_M781}	CGTAAGaAAG	GTCAACAAAT	AACITTTcTTT	GAAACAAAGc	AAGATTAcCC	
msa323014.2{343_2603}	CGTAAGaAAG	GTCAACAAAT	AACITTTcTTT	GAAACAAAGc	AAGATTAcCC	
msa323014.2{343_1169NT}	CGTAAGaAAG	GTCAACAAAT	AACITTTcTTT	GAAACAAAGc	AAGATTAcCC	
msa323014.2{343_090}	CGTAAGaAAG	GTCAACAAAT	AACITTTcTTT	GAAACAAAGc	AAGATTAcCC	
msa323014.2{343_CJB110}	CGTAAGaAAG	GTCAACAAAT	AACITTTcTTT	GAAACAAAGc	AAGATTAcCC	
msa323014.2{343_H36B}	CGTAAGcAAG	GTCAACAAAT	AACITTTcTTT	GAAACAAAGc	AAGATTAcCC	
msa323014.2{343_JM9130013}	CGTAAGcAAG	GTCAACAAAT	AACITTTcTTT	GAAACAAAGc	AAGATTAcCC	
Consensus	*****_***	*****	*****_***	*****_***	*****_***	*****_***
msa323014.2{343_18RS21}	501	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA
msa323014.2{343_A909}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA	
msa323014.2{343_COH1}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA	
msa323014.2{343_M732}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA	
msa323014.2{343_M781}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA	
msa323014.2{343_2603}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA	
msa323014.2{343_1169NT}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA	
msa323014.2{343_090}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA	
msa323014.2{343_CJB110}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA	
msa323014.2{343_H36B}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA	
msa323014.2{343_JM9130013}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCTAA	
Consensus	*****	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	551	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
msa323014.2{343_A909}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA	
msa323014.2{343_COH1}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA	
msa323014.2{343_M732}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA	
msa323014.2{343_M781}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA	
msa323014.2{343_2603}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA	
msa323014.2{343_1169NT}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA	
msa323014.2{343_090}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA	
msa323014.2{343_CJB110}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA	
msa323014.2{343_H36B}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA	
msa323014.2{343_JM9130013}	AACACATGAA	AGAGATTTAc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA	
Consensus	*****	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	601	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT
msa323014.2{343_A909}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT	
msa323014.2{343_COH1}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT	
msa323014.2{343_M732}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT	
msa323014.2{343_M781}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT	
msa323014.2{343_2603}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT	
msa323014.2{343_1169NT}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT	
msa323014.2{343_090}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT	
msa323014.2{343_CJB110}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT	
msa323014.2{343_H36B}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT	
msa323014.2{343_JM9130013}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCAACTTTT	
Consensus	*****	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	651	AGaGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_A909}	AGaGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG	
msa323014.2{343_COH1}	AGaGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG	
msa323014.2{343_M732}	AGaGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG	
msa323014.2{343_M781}	AGaGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG	
msa323014.2{343_2603}	AGaGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG	
msa323014.2{343_1169NT}	AGaGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG	
msa323014.2{343_090}	AGgGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG	
msa323014.2{343_CJB110}	AGgGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG	
msa323014.2{343_H36B}	AGgGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG	
msa323014.2{343_JM9130013}	AGgGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG	
Consensus	**..*****	*****_****	*****	*****	*****	*****
msa323014.2{343_18RS21}	701	ATGGTAAGAG	AGATACcGAG	CGAGTGAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_A909}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAG	ACAGTAGCCA	ACAAGATCCA	
msa323014.2{343_COH1}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAG	ACAGTAGCCA	ACAAGATCCA	
msa323014.2{343_M732}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAG	ACAGTAGCCA	ACAAGATCCA	
msa323014.2{343_M781}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAG	ACAGTAGCCA	ACAAGATCCA	
msa323014.2{343_2603}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAG	ACAGTAGCCA	ACAAGATCCA	

Table 74: Comparative Sequences relating to SAG1572

msa323014.2{343_1169NT}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_090}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_CJB110}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_H36B}	ATGGTAAGAG	AGATACtGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_JM9130013}	ATGGTAAGAG	AGATACtGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
Consensus	*****	*****_***	*****	*****	*****
751					
msa323014.2{343_18RS21}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_A909}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_COH1}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_M732}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_M781}	cTAGTATTAG	TAAA-----	-----	-----	-----
msa323014.2{343_2603}	cTAGTATTAG	TAAAagaata	tatcgctaata	ggtgataaaa	ctaatacaagc
msa323014.2{343_1169NT}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_090}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_CJB110}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_H36B}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_JM9130013}	gTAGTATTAG	TAA-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
801					
msa323014.2{343_18RS21}	-----	-----	-----	-----	-----
msa323014.2{343_A909}	-----	-----	-----	-----	-----
msa323014.2{343_COH1}	-----	-----	-----	-----	-----
msa323014.2{343_M732}	-----	-----	-----	-----	-----
msa323014.2{343_M781}	-----	-----	-----	-----	-----
msa323014.2{343_2603}	gataaaaaaa	gtagcaaaag	aatttaattct	caatagacaa	gaactctatg
msa323014.2{343_1169NT}	-----	-----	-----	-----	-----
msa323014.2{343_090}	-----	-----	-----	-----	-----
msa323014.2{343_CJB110}	-----	-----	-----	-----	-----
msa323014.2{343_H36B}	-----	-----	-----	-----	-----
msa323014.2{343_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
851					
msa323014.2{343_18RS21}	-----	-----	-----	-----	-----
msa323014.2{343_A909}	-----	-----	-----	-----	-----
msa323014.2{343_COH1}	-----	-----	-----	-----	-----
msa323014.2{343_M732}	-----	-----	-----	-----	-----
msa323014.2{343_M781}	-----	-----	-----	-----	-----
msa323014.2{343_2603}	ctagtttcca	tgattta	-----	-----	-----
msa323014.2{343_1169NT}	-----	-----	-----	-----	-----
msa323014.2{343_090}	-----	-----	-----	-----	-----
msa323014.2{343_CJB110}	-----	-----	-----	-----	-----
msa323014.2{343_H36B}	-----	-----	-----	-----	-----
msa323014.2{343_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	-----	-----	-----
851					
msa323014.2{343_18RS21}	-----	-----	-----	-----	-----
msa323014.2{343_A909}	-----	-----	-----	-----	-----
msa323014.2{343_COH1}	-----	-----	-----	-----	-----
msa323014.2{343_M732}	-----	-----	-----	-----	-----
msa323014.2{343_M781}	-----	-----	-----	-----	-----
msa323014.2{343_2603}	ctagtttcca	tgattta	-----	-----	-----
msa323014.2{343_1169NT}	-----	-----	-----	-----	-----
msa323014.2{343_090}	-----	-----	-----	-----	-----
msa323014.2{343_CJB110}	-----	-----	-----	-----	-----
msa323014.2{343_H36B}	-----	-----	-----	-----	-----
msa323014.2{343_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	-----	-----	-----

SEQ ID NO. 7412

STRAIN 2603 frame: 1

MEMQVQKSFKSNHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHF
DITTKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPISIDPGHDLVKAIEGDI PV
VSI PGASAGITALIASGLAPQPHI FYGFLPRKKGQITFFETKQDYPETQI FYESPFRVS
DTLKHMKIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDT
RVDSSQDPLVLVKEIYANGDKTNQAIKKVAKEFNLNRQELYAFHDL

SEQ ID NO. 7413

STRAIN 090 frame: 1

EMQVQKSFKSNHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHF
ITTKQISFHEHNAYDKISGLIDLKKEGRSLAQVSDAGMPISIDPGHDLVKAIEGGI PVV
SIPGASAGITALIASGLAPQPHI FYGFLPRKKGQITFFETKQDYPETQI FYESPFRVSD
TLKHMKIYGRQVVLVRELTKLYEYQRTISQLLGHIEKVPLKGECLIIVDGKRDT
VKDSSQDPLVLV

SEQ ID NO. 7414

STRAIN A909 frame: 2

VQKSFKSNHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHF
DITTKQISFHEHNAYDKISGLIDLKKEGRSLAQVSDAGMPISIDPGHDLVKAIEGDI PVV
SIPGASAGITALIASGLAPQPHI FYGFLPRKKGQITFFETKQDYPETQI FYESPFRVSD
TLKHMKIYGRQVVLVRELTKLYEYQRTISQLLGHIEKVPLKGECLIIVDGKRDT
VKDSSQDPLVLV

SEQ ID NO. 7415

STRAIN H36B frame: 1

EMQVQKSFKSNHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHF
ITTKQISFHEHNAYDKISGLIDLKKEGRSLAQVSDAGMPISIDPGHDLVKAIEGDI PVV
SIPGASAGITALIASGLAPQPHI FYGFLPRKKGQITFFETKQDYPETQI FYESPFRVSD
TLKHMKIYGRQVVLVRELTKLYEYQRTISQLLGHIEKVPLKGECLIIVDGKRDT
VKDSSQDPLVLV

SEQ ID NO. 7416

Table 74: Comparative Sequences relating to SAG1572

STRAIN 18RS21 frame: 1
 EMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 ITTKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDTER
 VKDSSQQDPLVLV

SEQ ID NO. 7417
 STRAIN M732 frame: 1
 EMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 ITTKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDTER
 VKDSSQQDPLVLV

SEQ ID NO. 7418
 STRAIN COH1 frame: 1
 EMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 ITTKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDTER
 VKDSSQQDPLVLV

SEQ ID NO. 7419
 STRAIN M781 frame: 3
 MQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDI
 TTKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVVS
 IPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSDT
 LKHMKEIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDTERV
 KDSSQQDPLVLV

SEQ ID NO. 7420
 STRAIN CJB110 frame: 1
 EMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 ITTKQISFHEHNAYDKISGLIDLKKEGRSLAQVSDAGMPSISDPGHDLVKAIEGGI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGRQVVLVRELTKLYEYQRTISQLLGHIEKVPLKGECLIIVDGKRDTER
 VKDSSQQDPLVLV

SEQ ID NO. 7421
 STRAIN 1169NT frame: 3
 QVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDIT
 TKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVVSI
 FGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSDTL
 KHMKEIYGRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDTERVK
 DSSQQDPLVLV

SEQ ID NO. 7422
 STRAIN JM9130013 frame: 1
 EMQVQKSFKSNHYGTLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
 ITTKQISFHEHNAYDKISGLIDLKKEGRSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
 TLKHMKEIYGRQVVLVRELTKLYEYQRTISQLLGHIEKVPLKGECLIIVDGKRDTER
 VKDSSQQDPVVLV

msa324064.2{343_18RS21}	1	-emqVQKSFK	SNiHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT	50
msa324064.2{343_A909}		----VQKSFK	SNiHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT	
msa324064.2{343_M781}		---mqVQKSFK	SNiHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT	
msa324064.2{343_2603}		memqVQKSFK	SNiHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT	
msa324064.2{343_COH1}		-emqVQKSFK	SNiHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT	
msa324064.2{343_M732}		-emqVQKSFK	SNiHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT	
msa324064.2{343_1169NT}		---qVQKSFK	SNtHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT	
msa324064.2{343_090}		-emqVQKSFK	SNtHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT	
msa324064.2{343_CJB110}		-emqVQKSFK	SNtHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT	
msa324064.2{343_H36B}		-emqVQKSFK	SNtHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT	
msa324064.2{343_JM9130013}		-emqVQKSFK	SNtHYGTLYL	VPTPIGNLDD	MTFRAIRILR	EVDFICAEDT	
Consensus		*--*-----	**-----	*****	*****	*****	
msa324064.2{343_18RS21}	51	RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLKKEGKS	LAQVSDAGMP	100
msa324064.2{343_A909}		RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLKKEGKS	LAQVSDAGMP	
msa324064.2{343_M781}		RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLKKEGKS	LAQVSDAGMP	
msa324064.2{343_2603}		RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLKKEGKS	LAQVSDAGMP	
msa324064.2{343_COH1}		RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLKKEGKS	LAQVSDAGMP	
msa324064.2{343_M732}		RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLKKEGKS	LAQVSDAGMP	
msa324064.2{343_1169NT}		RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLKKEGKS	LAQVSDAGMP	
msa324064.2{343_090}		RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLKKEGKS	LAQVSDAGMP	
msa324064.2{343_CJB110}		RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLKKEGKS	LAQVSDAGMP	
msa324064.2{343_H36B}		RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLKKEGKS	LAQVSDAGMP	
msa324064.2{343_JM9130013}		RNTGLLLKHF	DITTKQISFH	EHNAYDKISG	LIDLKKEGKS	LAQVSDAGMP	
Consensus		*****	*****	*****	*****	*****	

Table 74: Comparative Sequences relating to SAG1572

	101			150
msa324064.2{343_18RS21}	SISDPGHDLV KAAIEGdIPV VSIPGASAGI TALIASGLAP QPHIFYGFLP			
msa324064.2{343_A909}	SISDPGHDLV KAAIEGdIPV VSIPGASAGI TALIASGLAP QPHIFYGFLP			
msa324064.2{343_M781}	SISDPGHDLV KAAIEGdIPV VSIPGASAGI TALIASGLAP QPHIFYGFLP			
msa324064.2{343_2603}	SISDPGHDLV KAAIEGdIPV VSIPGASAGI TALIASGLAP QPHIFYGFLP			
msa324064.2{343_COH1}	SISDPGHDLV KAAIEGdIPV VSIPGASAGI TALIASGLAP QPHIFYGFLP			
msa324064.2{343_M732}	SISDPGHDLV KAAIEGdIPV VSIPGASAGI TALIASGLAP QPHIFYGFLP			
msa324064.2{343_1169NT}	SISDPGHDLV KAAIEGdIPV VSIPGASAGI TALIASGLAP QPHIFYGFLP			
msa324064.2{343_090}	SISDPGHDLV KAAIEGgIPV VSIPGASAGI TALIASGLAP QPHIFYGFLP			
msa324064.2{343_CJB110}	SISDPGHDLV KAAIEGgIPV VSIPGASAGI TALIASGLAP QPHIFYGFLP			
msa324064.2{343_H36B}	SISDPGHDLV KAAIEGdIPV VSIPGASAGI TALIASGLAP QPHIFYGFLP			
msa324064.2{343_JM9130013}	SISDPGHDLV KAAIEGdIPV VSIPGASAGI TALIASGLAP QPHIFYGFI.P			
Consensus	*****_***	*****	*****	*****
	151			200
msa324064.2{343_18RS21}	RKkGQQITFF ETkQdYPETQ IFYESPPFRVS DTLKHMKEIY GDRQVVLVRE			
msa324064.2{343_A909}	RKkGQQITFF ETkQdYPETQ IFYESPPFRVS DTLKHMKEIY GDRQVVLVRE			
msa324064.2{343_M781}	RKkGQQITFF ETkQdYPETQ IFYESPPFRVS DTLKHMKEIY GDRQVVLVRE			
msa324064.2{343_2603}	RKkGQQITFF ETkQdYPETQ IFYESPPFRVS DTLKHMKEIY GDRQVVLVRE			
msa324064.2{343_COH1}	RKkGQQITFF ETkQdYPETQ IFYESPPFRVS DTLKHMKEIY GDRQVVLVRE			
msa324064.2{343_M732}	RKkGQQITFF ETkQdYPETQ IFYESPPFRVS DTLKHMKEIY GDRQVVLVRE			
msa324064.2{343_1169NT}	RKkGQQITFF ETkQdYPETQ IFYESPPFRVS DTLKHMKEIY GDRQVVLVRE			
msa324064.2{343_090}	RKkGQQITFF ETkQdYPETQ IFYESPPFRVS DTLKHMKEIY GDRQVVLVRE			
msa324064.2{343_CJB110}	RKkGQQITFF ETkQdYPETQ IFYESPPFRVS DTLKHMKEIY GDRQVVLVRE			
msa324064.2{343_H36B}	RKkGQQITFF ETkQdYPETQ IFYESPPFRVS DTLKHMKEIY GDRQVVLVRE			
msa324064.2{343_JM9130013}	RKkGQQITFF ETkQdYPETQ IFYESPPFRVS DTLKHMKEIY GDRQVVLVRE			
Consensus	***_*****	*****	*****	*****
	201			250
msa324064.2{343_18RS21}	LTKLYEEYQR GTISQLLeHI EKVPLKGECL IIVDGKRDTE RVKDSSQQDP			
msa324064.2{343_A909}	LTKLYEEYQR GTISQLLeHI EKVPLKGECL IIVDGKRDTE RVKDSSQQDP			
msa324064.2{343_M781}	LTKLYEEYQR GTISQLLeHI EKVPLKGECL IIVDGKRDTE RVKDSSQQDP			
msa324064.2{343_2603}	LTKLYEEYQR GTISQLLeHI EKVPLKGECL IIVDGKRDTE RVKDSSQQDP			
msa324064.2{343_COH1}	LTKLYEEYQR GTISQLLeHI EKVPLKGECL IIVDGKRDTE RVKDSSQQDP			
msa324064.2{343_M732}	LTKLYEEYQR GTISQLLeHI EKVPLKGECL IIVDGKRDTE RVKDSSQQDP			
msa324064.2{343_1169NT}	LTKLYEEYQR GTISQLLeHI EKVPLKGECL IIVDGKRDTE RVKDSSQQDP			
msa324064.2{343_090}	LTKLYEEYQR GTISQLLgHI EKVPLKGECL IIVDGKRDTE RVKDSSQQDP			
msa324064.2{343_CJB110}	LTKLYEEYQR GTISQLLgHI EKVPLKGECL IIVDGKRDTE RVKDSSQQDP			
msa324064.2{343_H36B}	LTKLYEEYQR GTISQLLgHI EKVPLKGECL IIVDGKRDTE RVKDSSQQDP			
msa324064.2{343_JM9130013}	LTKLYEEYQR GTISQLLgHI EKVPLKGECL IIVDGKRDTE RVKDSSQQDP			
Consensus	*****_**	*****	*****	*****
	251			289
msa324064.2{343_18RS21}	lVLV-----	-----	-----	-----
msa324064.2{343_A909}	lVLV-----	-----	-----	-----
msa324064.2{343_M781}	lVLV-----	-----	-----	-----
msa324064.2{343_2603}	lVLVkeyian	gdktngaiikk	vakefnlnrq	elyasfhdI
msa324064.2{343_COH1}	lVLV-----	-----	-----	-----
msa324064.2{343_M732}	lVLV-----	-----	-----	-----
msa324064.2{343_1169NT}	lVLV-----	-----	-----	-----
msa324064.2{343_090}	lVLV-----	-----	-----	-----
msa324064.2{343_CJB110}	lVLV-----	-----	-----	-----
msa324064.2{343_H36B}	lVLV-----	-----	-----	-----
msa324064.2{343_JM9130013}	vVLV-----	-----	-----	-----
Consensus	-*****	*****	*****	*****

Table 75: Comparative Sequences relating to SAG0671

SEQ ID NO. 7501
STRAIN 2603
ATGAGCGTATATGTTAGTGGAAATAGGAATTATT
TCTTCTTTGGGAAAGAATTATAGCGAGCATAAACAGCATCTCTTCGACTTAAAGAAGGA
ATTTCTAAACATTTATATAAAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATA
ACTAGTGACCCAGAGGTTCTCTGAGCAATACAAAGATGAGACACGTAATTTAAATTTGCT
TTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTTAAAGCTTATCATAT
ATTGCTGTGTGTTTAGGACCTCACTTGGGGGAAAGAGTGCTGGTCAAATGCCTTGAT
CAATTTGAAGAAGGAGAGCGTCAAGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTAC
CATATTGCTGATGAATTTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTC
ACCGCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAAGATGGC
GATTGTGATTTAGCTATTTTGGTGGCTGTGATGAGTTAAGTGATATTTCTTTAGCAGGC
TTCACATCACTAGGAGCTATTAATACAGAAATGGCATGTGAGCCCTATTCTTCTGGAAAA
GGAATCAATTTGGGTGAGGGCGCTGTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCT
AAATATGAAAAATTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCT
AAGCCAACAGGTGAAGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCAGGTATT
GACTACAGTGAGATTGACTATATTAAACGGTCACGGTACAGGTACTCAAGCTAATGATAAA
ATGAAAAAAATATGATGTAAGTTTTCGCCACAACGACATTGATCAGCAGTACCAAG
GGGCAACGGGTCATAGCTCTAGGGGCTGACAGGTATTATCGAATTGATTAAATGTTTAGCG
GCAATAGAGGAACAGACTGTACCACTAAATGAGATTGGGATAGAAGGTTTTCCA
GAAAAATTTGTCTATCATCAAAGAGAGAATACCCAATAAGAAATGCTTTAAATTTTTCG
TTTGTCTTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCTTTAGATTCACTCTAGAA
ACATTACCTGCTAGAGAAATCTTAAATGGCTATCTTATCATCTGTGCTTCCATTCT
AAGAATGAATCATTCTTATTAACCTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAA
GCATTACGCTTTAAAGGGGCTAGACCACCAAACTGTCAACCCAGCACAAATTTAGGAAA
ATGATGATTTTTCCAAAATGGTGGCGTAACACAGCTCAAGCACTAATAGAAAGCAAT
ATTAATCTAAAAAAACAGATACTTCAAAGTAGGAATTTGATTTACAACACTTTCTGGA
CCAGTTGAGGTTGTTGAAGGTATTGAAAAAGCAATCAACAAGAGGATATGCACATGTT
TCTGCTTCAGCATTCCTGTTTACAGTAATGAGTGCAGCAGCTGGTATGCTTTCTATCATT
TTTAAAAATAACAGGTCCTTTATCTGTCTTTTCGACAAATAGTGGAGCGCTTGATGGTATA
CAATATGCCAAGGAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTCTCTGCT
AATCAGTGGACAGACAGATTTTATGTGGTGGCAACAATTAACATATGATAGTCAAATG
TTTGTGCGTTCTGATTATTGTTTCAGCACAAAGTCTCTCTCGTCAAGCATTTGGATAATTCT
CCTATAATATTAGGTAGTAACAATTAATAATAGCCATAAAACATTACAGATGTGATG
ACTATTTTGTGCTGCTGCGCTCAAATTTATTTATCAGACTTAGGACTAACCATAAAAGAT
ATCAAAGGTTTCGTTTGAATGAGCGGAAGAGGAGGAGTTAGTTTCAAGATTATGATTTCTTA
GCGAATCTGTCTGATATTATAATATGCCAAACCTTGCTTCTGGTCAGTTTGGATTTTCA
TCTAATGCTGCTGGTGAAGAAGTGGACTATAGTTAATGAAAGTATAGAAAAGGCTAT
TATTAGTCTATCTTATTCGATCTTCGGTGGTATCTCTTTGCTATTATTGAAAAAGG

SEQ ID NO. 7502
STRAIN 090
ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGaATTAT
AGCGAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACA
TTTATATAAAATCAAGACTCTATTTTAGAATCTTATACAGGAAGCATAA
CTAGTGACCCAGAGGTTCTCTGAGCAATACAAAGATGAGACACGTAATTTT
AAATTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAA
TTTAAAAAGCTTATCATAATATGCTGTGTGTTTAGGGACCTCACTTGGGG
GAAAGAGTGCTGGTCAAATGCCITGTATCAATTTGAAGAAGGAGAGCGT
CAAGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGA
TGAATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAA
CCGCCCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTT
CAAGATGGCGAATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAG
TGATATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTATACAGAAA
TGGCATGTGAGCCCTATTCTTCTGAAAAAGGAATCAATTTGGGTGAGGGC
GCTGGTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAATATGGA
AATTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTA
AGCCAACAGGTGAAGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAA
GCAGGTATTGACTACAGTGAGATTGACTATATTAAACGGTCACGGTACAGG
TACTCAAGCTAATGATAAAATGGAAGAAAAATATGATGGTAAGTTTTC
CGACAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCACTACTA
GGGGCTGCAGGTATTATCGAATTGATTAAATGTTTAGCGGCAATAGAGGA
ACAGACTGTACCAAGCACTAAATGAGATTGGGATAGAAGGTTTTCCAG
AAAAATTTGTCTATCATCAAAGAGAGAATACCCAATAAGAAATGCTTTA
AATTTTCTGTTTGTCTTTGGTGGAAATAATAGTGGTATCTTATTGTCATC
TTTAGATTCACTCTAGAAACATTACCTGCTAGAGAAAATCTTAAATG
CTATCTTATCATCTGTTGCTTCCATTCTAAGAAATGAATCACTTTCTATA
ACCTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTT
TAAAGGGGCTAGACCACCAAACTGTCAACCCAGCACAAATTTAGGAAAA
TGGATGATTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATA
GAAAGCAATATTAACTAAAAAAACAAGTACTTCAAAGTAGGAATGTT
ATTTACAACACTTTCTGGACAGTTGAGGTGTTGAAGGTATTGAAAGC
AAATCACAACAGAGGATATGCACATGTTTCTGCTTCAGGATTCCTGTTT
ACAGTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTAAAAATAAC
AGGTCTTTATCTGCTATTTGACAAATAGTGGAGCGCTTGATGGTATAC
AATATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTT
GTTTCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAAAT
AACTATGATAGTCAAATGTTTGTGCGTTCTGATTATTGTTTCAGCACAAG
TCCTCTCTCGTCAAGCATTTGGATAATTCTCCTATAATATTAGGTAGTAAA
CAATTAATAATAGCCATAAAACATTACAGATGTGATGACTATTTTGA
TGCTGCGCTTCAAATTTATTTATCAGACTTAGGACTAACCATAAAAGATA
TCAAAGGTTTCGTTTGAATGAGCGGAAGAGGAGTTAGTTCAAGATTAT
GATTTCTTAGCGAATCTGTCTGAGTATTATAATATGCCAAACCTTGCTTC

Table 75: Comparative Sequences relating to SAG0671

TGGTCAGTTTGGATTTTCATCTAATGGTGTGGTGAAGAAGTGGACTATA
CTGTTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTATCTTATTCG
ATCTTTGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7503

STRAIN A909

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATT
ATAGCGAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAA
CAITTTATATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCAT
AACTAGTGACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATT
TTAAATTTGCTTTTACCCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTT
AATTTAAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGG
GGGAAAGAGTGTGGTCAAAATGCCCTGTATCAATTTGAAGAAGGAGAGC
GTCAAGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCT
GATGAATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTT
AACCGCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTAC
TTCAGATAGGCGATTGTGATTAGCTATTGTGGTGGCTGTGATGAGTTA
AGTGATATTTCTTTAGCAGGCTTCAATCACTAGGAGCTATTAATACAGA
AATGGCATGTGAGCCCTATTCTTCTGAAAAGGAATCAATTTGGGTGAGG
GCGCTGGTTTGTGTCTTGTCAAAGATCAGTCTTCTAGCTAAATATGGA
AAAATTTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACC
TAAGCCAACAGGTGAAGGGGCGGCACAGATTGCAAGCAGCTAGTGACTC
AAGCAGGTATTGACTACAGTGAGATTGACTATATTAAACGGTCACGGTACA
GGTACTCAAGCTAATGATAAATGGAATAATATGTTATGTTAAGTTT
CCCGACAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCACTACTC
TAGGGGCTGACAGTATTATCGAATTGATTAAATGTTTAGCGGCAATAGAG
GAACAGACTGTACAGCAACTAAAAATGAGATTGGGATAGAAGGTTTCC
AGAAAATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTT
TAAATTTTCTGTTTGTCTTTTGGTGGAAATAATAGTGGTGTCTTATTGTCA
TCTTTAGATTCACTCTAGAAAACATTACCTGCTAGAGAAAAATCTTAAAT
GGCTATCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTA
TAACCTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGC
TTTAAAGGGGCTAGACCACCCAAACTGTCAACCCAGCACATTTAGGAA
AATGGATGATTTTCCAAAATGGTTGCCGTAAACAGCTCAAGCACTAA
TAGAAAGCAATAATTAATCTAAAAAACAAGATACTTCAAAAGTAGGAATT
GTATTTACAAACATTTCTGACCAGTTGAGGTTGTGAAGGTATTGAAAA
GCAATCACAACAGAAAGGATATGCATGTTTCTGCTTCAAGATTCCCGT
TTACAGTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTAAAATA
ACAGGTCCTTTATCTGTCTATTTCGACAAATAGTGGAGCGCTTGATGGTAT
ACAATATGCCAAGGAAATGATGCGTAAACGATAATCTAGACTATGTGATTC
TTGTTTCTGCTAATCAGTGGACAGACATGAGTTTATGTGTGGGCAACA
TTAACTATGATAGTCAAAATGTTTGTCCGTTCTGATTATTGTTCAAGACA
AGTCTCTCTCTCGTCAAGCATTGGATAAATCTCTATAATATTAGGTAGTA
AACAAATAAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTT
GATGCTGCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAAGA
TATCAAGGTTTCTGTTTGAATGAGCGGAAGAAGGCAGTTAGTTCAAGATT
ATGATTTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCT
TCTGGTCAAGTTTGGATTTCATCTAATGGTGTGGTGAAGAAGCTGGACTA
TACTGTTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTCTATCTTATT
CGATCTTCCGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7504

STRAIN H36B

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGCGA
GCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATTAT
ATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCATAACTAGT
GACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATTTTAAATT
TGCTTTTACCCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTTAA
AAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAAAG
AGTGTGTTGTTCAAAATGCCCTGTATCAATTTGAAGAAGGAGAGCGTCAAGT
AGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATGAAT
TGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCGCC
TGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAAGA
TGGCGATTGTGATTAGCTATTGTGGTGGCTGTGATGAGTTAAGTGATA
TTTCTTTAGCAGGCTTCAATCACTAGGAGCTATTAAATACAGAAATGGCA
TGTCAGCCCTATTCTTCTGAAAAGGAATCAATTTGGGTGAGGGCGCTGG
TTTTGTGTCTTGTCAAAGATCAGTCTTCTAGCTAAATATGGAATAATTA
TCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGCCA
ACAGGTGAAGGGGCGGCACAGATTGCAAGCAGCTAGTGACTCAAGCAGG
TATTGACTACAGTGAGATTGACTATATTAAACGGTCACGGTACAGGTACTC
AAGCTAATGATAAATGGAATAAATATGTTATGTTAAGTTTCTCCGACA
ACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCACTCTAGGGGC
TGCAGGTATTATCGAATTGATTAAATGTTTAGCGGCAATAGAGGAACAGA
CTGTACCAAGCAACTAAAAATGAGATTGGGATAGAAGGTTTCCAGAAAAAT
TTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAATTT
TTCGTTTGTCTTTGGTGGAAATAATAGTGGTGTCTTATTGTCTATCTTTAG
ATTCACTCTAGAAAAATTTACCTGCTAGAGAAAAATCTTAAATGGCTATC
TTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACCTA
TGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAAAG
GGGCTAGACCACCCAAACTGTCAACCCAGCACAAATTTAGGAAAATGGAT
GATTTTTTCCAAAATGGTTGCCGTAAACAGCTCAAGCACTAATAGAAAAG
CAATATTAACTCAAAAAAACAAGATACTTCAAAAGTAGGAATTGTATTTA
CAACACTTTCTGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAATC

Table 75: Comparative Sequences relating to SAG0671

ACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGTTTACAGT
AATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAATAACAGGTC
CTTTATCTGTCTATTTCCGACAAATAGTGGAGCGCTTGATGGTATACAAAT
GCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTTCTGTTTC
TGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAACT
ATGATAGTCAAATGTTTGTGCGTTCTGATTATTGTTCCAGCACAAGTCCTC
TCTCGTCAAGCATTGGATAATTCTCTATAATATTAGGTAGTAAACAATT
AAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGTATGCTG
CGCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCAAA
GGTTTCGTTTGAATGAGCGGAAGAGGAGGAGTTAGTTTATGATTTT
CTTAGCGAATCTGTCTGAGTATTATAATATGCCAACCTTGCTTCTGGTC
AGTTTGGATTTTCTATCTAATGGTGTGCTGGTGAAGAACTGGACTATCTGTT
AATGAAAGTATAGAAAAGGGCTATTATTAGTCTTATCTTATCGATCTT
CGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7505

STRAIN 18RS21

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
GAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACATTT
ATATAAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAACTA
GTGACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATTTTAA
TTTGCTTTTACCCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTT
AAAAGCTTATCATAATATTGCTGTGTGTTAGGGACCTCAGTTGGGGGA
AGAGTGTGCTGCTCAAAATGCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
GTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATGA
ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCG
CCTGTTCTGCAAGTAATAATGCGTAATAATTAGGAACACAATTACTTCAA
GATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
TATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAAATACAGAAATGG
CATGTCAGCCCTATTCTTCTGGAAGGAATCAATTTGGGTGAGGGCGCT
GGTTTGTGTTCTTGTCAAAGATCAGTCTCTAGCTAAATATGGAATAAT
TATCGGTGCTTATTACTTTCAGATGGTTATCATATAACAGCACCTTAAGC
CAACAGGTGAAGGGGCGGCACAGATTGCAAGCAGCTAGTGACTCAAGCA
GGTATTGACTACAGTGAGATTGACTATTTAACGGTCAAGGTACAGGTAC
TCAAGCTAATGATAAAATGGAATAAATATGTATGGTAAGTTTTCCTCGA
CAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCTACTCTAGGG
GCTGCAAGTATTATCGAATTGATTAAATGTTTAGCGGCAATAGAGGAACA
GACTGTACAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCAGAAA
ATTTTGTCTATCATCAAAGAGAGAAATACCAATAAGAAATGCTTTAAAT
TTTTGCTTTGCTTTTGGTGAATAATAGTGGTGTCTTATTGTCTATCTTT
AGATTACCTCTAGAAACATTACCTGCTAGAGAAATCTTAAATGGCTA
TCTTATCATCTGTGCTTCCATTTCTAAGAAATGAATCACTTTCTATAACC
TATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
AGGGGCTAGACCCCAAACTGTCAACCCAGCACAATTTAGGAAAATGG
ATGATTTTTCCAAAATGGTTGCGGTAAACAGCTCAAGCACTAATAGAA
AGCAATATTAACTTAAAAAACAAGATACTTCAAAGTAGGAATTGTATT
TACAACACTTTCTGGACAGTTGAGGTGTTGAAGGTATTGAAAAGCAAA
TCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCGTTTACA
GTAATGAATGCAAGCAGCTGGTATGCTTTCTATCATTTTAAATAACAGG
TCCTTTATCTGTCATTTGCAAAATAGTGGAGCGCTTGATGGTATACAAT
ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTT
TCTGTCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTA
CTATGATGTCAAATGTTTGTGCGTTCTGATTATTGTTCCAGCACAAGTCC
TCTCTCGTCAAGCATTGGATAATTCTCTATAATATTAGGTAGTAAACAA
TTAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGTATGCT
TGCGCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCA
AAGGTTTCTGTTTGAATGAGCGGAAGAGGAGGAGTTAGTTTATGATGAT
TTCTTAGCGAATCTGTCTGAGTATTATAATATGCCAACCTTGCTTCTGG
TCAGTTTGGATTTTCTATCTAATGGTGTGCTGGTGAAGAACTGGACTATCTG
TTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTTATCTTATCGATCT
TTCGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7506

STRAIN M732

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAG
CGAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACATT
TATATAAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAACT
AGTGACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATTTTAA
ATTTGCTTTTACCCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTT
TAAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCAGTTGGGGGA
AAGAGTGTGCTGCTCAAAATGCTTGTATCAATTTGAAGAAGGAGAGCGTCA
AGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGATG
AATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACC
GCCTGTTCTGCAAGTAATAATGCCGTAATAATTAGGAACACAATTACTTCA
AGATGGCGATTGTGATTTAGCTATTGTTGGTGGCTGTGATGAGTTAAGTG
ATATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAAATACAGAAATG
GCATGTCAGCCCTATTCTTCTGGAAGGAATCAATTTGGGTGAGGGCGC
TGGTTTGTGTTCTTGTCAAAGATCAGTCTTCTAGCTAAATATGGAATAA
TTATCGGTGGTCTTATTACTTTCAGATGGTTATCATATAACAGCACCTTAAG
CCAACAGGTGAAGGGGCGGCACAGATTGCAAGCAGCTAGTGACTCAAGC
AGGTATTGACTACAGTGAGATTGACTATTTAACGGTCAAGGTACAGGTA
CTCAAGCTAATGATAAAATGGAATAAATATGTATGGTAAGTTTTCCTCG
ACAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCTACTCTAGG

Table 75: Comparative Sequences relating to SAG0671

GGCTGCAGGTATTATCGAATTGATTAATTGTTTAGCGGCAATAGAGGAAC
 AGACTGTACCAGCACTAAAAATGAGATTGGGATAGAAGGTTTCCAGAA
 AATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAA
 TTTTTCGTTTGGCTTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCT
 TAGATTACCTCTAGAAAACATTACCTGCTAGAGAAAATCTTAAATGGCT
 ATCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAAC
 CTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTA
 AAGGGGCTAGACCACCCAAAACCTGTCAACCCAGCACAATTTAGGAAAATG
 GATGATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGA
 AAGCAATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATTGTAT
 TTACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAA
 ATCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGTTTAC
 AGTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTTTAAATAACAG
 GTCCTTTATCTGTCATTTTCGACAAATAGTGGAGCGCTTGATGGTATACAA
 TATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGT
 TTCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAA
 ACTATGATAGTCAAAATGTTTGTGCGTTCTGATTATTGTTGAGCACAAGTC
 CTCTCTCGTCAAGCATTGGATAAATCTCTATAATATTAGGTAGTAAACA
 ATTAAATATAGCCATAAAACATTCACAGATGTGATGACTATTTTGTATG
 CTGCGCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATC
 AAAGGTTTCGTTTGAATGAGCGGAAGAAGGCAGTTAGTTGAGATTATGA
 TTTCTAGCGAAGCTTGTCTGAGTATTATAATATGCCAAACCTTGTCTCTG
 GTCAGTTTGGATTTCATCTAATGGTGTGCTGGAAGAACTGGACTataCT
 GTTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTCTATCTTATTCGAT
 CTTCCGGTGGTATCTCTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7507

STRAIN COH1

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
 GAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACATT
 ATATAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAACTA
 GTGACCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTTTAA
 TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTT
 AAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
 AGAGTGTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTTATTAGAAAAGCATCTGTTTACCATATTGCTGATGA
 ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCACCCG
 CCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAA
 GATGGCGATTGTGATTAGCTATTGTGGTGGCTGTGATGAGTTAAGTGA
 TATTTCTTTTAGCAGGCTTACATCACTAGGAGCTATTAATACAGAAATGG
 CATGTCAGCCCTATTCTTCTGAAAAGGAATCAATTTGGGTGAGGGCGCT
 GGTTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGAAAAAT
 TATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGC
 CAACAGGTGAAGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
 GGTATTGACTACAGTGAGATTGACTATATTACCGTCACGGTACAGGTAC
 TCAAGCTAATGATAAAATGAAAAAATATGTATGGTAAGTTTTCCTCGA
 CAACGACATTGATCAGCAGTACCAAGGGGCAACCGGTCATCTCTAGGG
 GCTGCAAGTATTATCGAATTGATTAAATGTTTAGCGGCAATAGAGGAACA
 GACTGTACCAGCACTAAAAATGAGATTGGGATAGAAGGTTTTCAGAAA
 ATTTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGCTTTAAAT
 TTTTCGTTTGGCTTTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCTT
 AGATTACCTCTAGAAAACATTACCTGCTAGAGAAAATCTTAAATGGCTA
 TCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACC
 TATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
 AGGGGCTAGACCACCCAAAACCTGTCAACCCAGCACAATTTAGGAAAATGG
 ATGATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAA
 AGCAATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATTGTATT
 TACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAAA
 TCACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCCGTTTACA
 GTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTTTAAATAACAGG
 TCCTTTATCTGTCATTTTCGACAAATAGTGGAGCGCTTGATGGTATACAA
 ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGT
 TCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAA
 CTATGATAGTCAAAATGTTTGTGCGTTCTGATTATTGTTGAGCACAAGTCC
 TCTCTCGTCAAGCATTGGATAAATCTCTATAATATTAGGTAGTAAACAA
 TTAATATATAGCCATAAAACATTCACAGATGTGATGACTATTTTGTATG
 TCGCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCA
 AAGGTTTCGTTTGAATGAGCGGAAGAAGGCAGTTAGTTGAGATTATGAT
 TTTCTAGCGAAGCTTGTCTGAGTATTATAATATGCCAAACCTTGTCTCTGG
 TCAGTTTGGATTTCATCTAATGGTGTGCTGGAAGAACTGGACTATCTG
 TTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTCTATCTTATTCGATC
 TCGGTGGTATCTCTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7508

STRAIN M781

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
 GAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACATT
 ATATAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAACTA
 GTGACCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTTTAA
 TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTT
 AAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
 AGAGTGTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTATTAGAAAAGCATCTGTTTACCATATTGCTGATGA

Table 75: Comparative Sequences relating to SAG0671

ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCG
 CCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAA
 GATGGCGATTGTGATTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
 TATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACAGAAATGG
 CATGTGAGCCCTATTCTCTGGAAAAGGAATCAATTTGGGTGAGGGCGCT
 GGTTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAATAAT
 TATCGGTGGTCTTATTAATTCAGATGGTTATCATATAACAGCACCTAAGC
 CAACAGGTGAAGGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
 GGTATTGACTACAGTGAGATTGACTATATTAATGGTCACGGTACAGGTAC
 TCAAGCTAATGATAAAATGGAATAAATATGTATGGTAAGTTTTCCCGA
 CAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCTACTCTAGGG
 GCTGCAGGTATTATCGAATTGATTAAATGTTTAGCGGCAATAGAGGAACA
 GACTGTACAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAAA
 ATTTTGTCTATCATCAAAAGAGAGAATACCAATAAGAAATGCTTTAAAT
 TTTTCGTTTGTCTTTGGTGGAAATAATAGTGGTATCTTATTGTCTATCTT
 AGATTACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAATGGCTA
 TCTTATCATCTGTTGCTTCCATTCTAAGAATGAATCACTTCTATAACC
 TATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
 AGGGGCTAGACCAACCAAACTGTCAACCCAGCACAAATTTAGGAAAATGG
 ATGATTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAA
 AGCAATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATGTATT
 TACAACACTTTCTGGACAGTTGAGGTTGTGAAGGTATTGAAAAGCAAA
 TCACAACAGAAGGATATGCACATGTTTCTGCTTACGATTCCCGTTTACA
 GTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTAAATAACAGG
 TCCCTTTATCTGTCTATTTCGACAAATAGTGGAGCGCTTGATGGTATACAAT
 ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTGTGT
 TCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAA
 CTATGATAGTCAAAATGTTTGTGGTCTGATTATTGTTTCAACAGTCC
 TCTCTCGTCAAGCATTGGGATAATCTCCTATAATATTAGGTAGTAAACAA
 TTAATAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGTATGC
 TGGCCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAGATATCA
 AAGGTTTCGTTTGGAAATGAGCGGAAGAAGGCAGTTAGTTTCAAGTTATGAT
 TTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGTCTCTGG
 TCAGTTTGGATTTCATCTAATGGTGTGGTGAAGAACTGGACTATAGTG
 TTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTCTATCTATTTCGATC
 TTTGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7509

STRAIN CJB110

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAAATTATAGC
 GAGCATAAAGCAGCATCTCTCGACTTAAAGAAAGGAATTTCTAAACATTT
 ATATAAAATCAGGACTCTATTTTGAATCTTATACAGGAAGCATAACTA
 GTGACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTTTAA
 TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGTCTTCTCAGGTGTTAATTT
 AAAAGCTTATCATAAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
 AGAGTGTGGTCAAAATGCCCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTTATTAGAAAAGCATCTGTTTACCATATTGCTGATGA
 ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTAATTTCAACCG
 CCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAA
 GATGGCGATTGTGATTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
 TATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAAATACAGAAATGG
 CATGTGAGCCCTATTCTCTGAAAAGGAATCAATTTGGGTGAGGGCGCT
 GGTTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAATAAT
 TATCGGTGGTCTTATTAATTCAGATGGTTATCATATAACAGCACCTAAGC
 CAACAGGTGAAGGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
 GGTATTGACTACAGTGAGATTGACTATATTAATGGTCACGGTACAGGTAC
 TCAAGCTAATGATAAAATGGAATAAATATGTATGGTAAGTTTTCCCGA
 CAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCTACTCTAGGG
 GCTGCAGGTATTATCGAATTGATTAAATGTTTAGCGGCAATAGAGGAACA
 GACTGTACAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAAA
 ATTTTGTCTATCATCAAAAGAGAGAATACCAATAAGAAATGCTTTAAAT
 TTTTCGTTTGTCTTTGGTGGAAATAATAGTGGTATCTTATTGTCTATCTT
 AGATTACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAATGGCTA
 TCTTATCATCTGTTGCTTCCATTCTAAGAATGAATCACTTCTATAACC
 TATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
 AGGGGCTAGACCAACCAAACTGTCAACCCAGCACAAATTTAGGAAAATGG
 ATGATTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAA
 AGCAATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATGTATT
 TACAACACTTTCTGGACAGTTGAGGTTGTGAAGGTATTGAAAAGCAAA
 TCACAACAGAAGGATATGCACATGTTTCTGCTTACGATTCCCGTTTACA
 GTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTAAATAACAGG
 TCCCTTTATCTGTCTATTTCGACAAATAGTGGAGCGCTTGATGGTATACAAT
 ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTGTGT
 TCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTAA
 CTATGATAGTCAAAATGTTTGTGGTCTGATTATTGTTTCAACAGTCC
 TCTCTCGTCAAGCATTGGGATAATCTCCTATAATATTAGGTAGTAAACAA
 TTAATAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGTATGC
 TGGCCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAGATATCA
 AAGGTTTCGTTTGGAAATGAGCGGAAGAAGGCAGTTAGTTTCAAGTTATGAT
 TTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGTCTCTGG
 TCAGTTTGGATTTCATCTAATGGTGTGGTGAAGAACTGGACTATAGTG
 TTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTCTATCTATTTCGATC
 TTTGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

Table 75: Comparative Sequences relating to SAG0671

SEQ ID NO. 7510

STRAIN 1169NT

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAG
 CGAGCATAAACAGCATCTCTTCGACTTAAAGAAAGGAATTTCTAAACATT
 TATATAAAAATCAGGACTCTATTTTAGAATCTTATACAGGAAGCATAACT
 AGTGACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATTTTAA
 ATTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATT
 TAAAAGCTTATCATAAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGA
 AAGAGTGTGGTCAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCA
 AGTAGATGCTAGTTTATAGAAAAAGCATCTGTTTACCATATTGCTGATG
 AATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACC
 GCCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCA
 AGATGGCGATTGTGATTAGCTATTGTGGTGGCTGTGATGAGTTAAGTG
 ATATTTCTTTAGCAGGCTTACATCACTAGGAGCTATTAATACAGAAATG
 GCATGTGAGCCCTATTCTTCTGGAAGAAAGGAATCAATTTGGGTGAGGGCGC
 TGGTTTGTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAGAAA
 TTATCGGTGGTCTTATTACTTTCAGATGGTTATCATATAACAGCACCTAAG
 CCAACAGGTGAAGGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGC
 AGGTATTGACTACAGTGAGATTGACTATATTACGGTCACGGTACAGGTA
 CTCAAGCTAATGATAAAATGGAAGAAATATGTTAGTTAAGTTTTCCTCG
 ACAACGACATTGATCAGCAGTACCAAGGGGCAACCGGTCATACTTAGG
 GGCTGCAGGTATTATCGAATTGATTAAATTGTTTAGCGGCAATAGAGGAAC
 AGACTGTACCAGCACTAAAAATGAGATTGGGATAGAAAGTTTTCAGAA
 AATTTTGTCTATCATCAAAGAGAGAATACCAATAAGAAATGCTTTAA
 TTTTTCGTTTGTCTTTGGTGGAAATAATAGTGGTATCTTATTGTCTATCT
 TAGATTCACTCTAGAAACATTACCTGCTAGAGAAATCTTAAATGGCT
 ATCTTATCATCTGTTGCTTCCATTCTAAGAATGAATCACTTTCTATAAC
 CTATGAAAAGTTGTAGTAATTTCAACGACTTTGAAGCAATTACGCTTTA
 AAGGGGCTAGACCACCCAAACTGTCAACCCAGCACAAATTTAGGAAATG
 GATGATTTTCCAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGA
 AAGCAATATTAATCTAAAAACAAGATACTTCAAAGTAGGAATTGTAT
 TTACAACACTTTCTGGACCAAGTTGAGGTTGTTGAAGGTATTGAAAAGCAA
 ATCACAACAGAAAGGATATGCACATGTTCTGCTTCACGATTCCCGTTTAC
 AGTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTAAATAACAG
 GTCCTTTATCTGTCAATTCGACAAATAGTGGAGCGCTTGATGGTATACAA
 TATGCCAAGGAATGATGCGTAACAGATAATCTAGACTATGTGATTCTTGT
 TTCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTA
 ACTATGATAGTCAAATGTTTGTGCGTTCTGATTATTGTTTCAACAGCTC
 CTCTCTCGTCAAGCAATTGGATAATTCTCCTATAATATTAGGTAGTAAACA
 ATTTAAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGTATG
 CTGCGCTTCAAATTTTATTATCAGACTTAGGACTAACCATAAAGATATC
 AAAGGTTTTCGTTTGGAAATGAGCGGAAGAAGGCAGTTAGTTTCAAGATTATGA
 TTTCTTAGCGAATCTGTCTGAGTATTATAATATGCCAACCTTGCTCTG
 GTCAGTTTGGATTTCATCTAATGGTGGCTGGTGAAGAACTGGACTATACT
 GTTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTTATCTTATTCGAT
 CTTTGGTGGTATCTCTTTTGGCTATTATTGAAAAAAG

SEQ ID NO. 7511

STRAIN JM9130013

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGCGAG
 CATAAACAGCATCTCTTCGACTTAAAGAAAGGAATTTCTAAACATTATATA
 TAAAAATCAGGACTCTATTTTAGAATCTTATACAGGAAGCATAACTAGTG
 ACCGAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATTTTAAATTT
 GCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTTAA
 AGCTTATCATAAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGAAAGA
 GTGCTGGTCAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAAGTA
 GATGCTAGTTTATAGAAAAAGCATCTGTTTACCATATTGCTGATGAATT
 GATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCGCTT
 GTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAAGAT
 GGCGATTGTGATTAGCTATTGTGGTGGCTGTGATGAGTTAAGTGATAT
 TTCTTTAGCAGGCTTACATCACTAGGAGCTATTAAACAGAAATGGCAT
 GTCAGCCCTATTCTTCTGGAAGAAAGGAATCAATTTGGGTGAGGGCGCTGGT
 TTTGTTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAGAAATAT
 CGGTGGTCTTATTACTTTCAGATGGTTATCATATAACAGCACCTAAGCCAA
 CAGGTGAAGGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCAGGT
 ATTGACTACAGTGAGATTGACTATATTACGGTCACGGTACAGGTACTCA
 AGCTAATGATAAAATGGAAGAAATATGTTAGTTAAGTTTTCCTCGACAA
 CGACATTGATCAGCAGTACCAAGGGGCAACCGGTCATACTCTAGGGGCT
 GCAGGTATTATCGAATTGATTAAATTGTTTAGCGGCAATAGAGGAACAGAC
 TGTACAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCAGAAAAAT
 TTGCTATCATCAAAGAGAGAATACCAATAAGAAATGCTTTAAATTTT
 TCGTTTGTCTTTGGTGGAAATAATAGTGGTGTCTTATTGTCTCTTTAGA
 TTCACCTCTAGAAACATTACCTGCTAGAGAAATCTTAAATGGCTATCT
 TATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACCTAT
 GAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCAATTACGCTTTAAGG
 GGCTAGACCACCCAAACCTGTCAACCCAGCACAAATTTAGGAAATGGATG
 ATTTTTCAAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAAAGC
 AATATTAAATCTAAAAACAAGATACTTCAAAGTAGGAATTGTATTAC
 AACACTTTCTGGACCAAGTTGAGGTTGTTGAAGGTATTGAAAAGCAATCA
 CAACAGAGGATATGCACATGTTCTGCTTCAAGATTCCCGTTTACAGTA
 ATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTAAATAACAGGTCC
 TTTATCTGTCAATTCGACAAATAGTGGAGCGCTTGATGGTATACAAATATG

Table 75: Comparative Sequences relating to SAG0671

CCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTTCCT
 GCTAATCAGTGGACAGACATGAGTTTATGTTGGTGGCAACAATTAACCTA
 TGATAGTCAAATCTTTGTCGGTTCTGATTATTGTTTACGACACAGTCCTCT
 CTCGTCAAGCATGGATAATTCTCCTATAATATTAGGTAGTAAACAATTA
 AAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGTGCTGCG
 GCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAGATATCAAAG
 GTTTCGTTTGAATGAGCGGAAGAGGCAGTTAGTTTCAAGATTATGATTTC
 TTAGCGAAGCTGTCTGAGTATTATAATATGCCAAACCTTGTCTCTGGTCA
 GTTTGGATTTCATCTAATGGTGTCTGGTGAAGAACTGGACTATACGTGA
 ATGAAAGTATAGAAAGGGCTATTATTAGTCCTATCTTATTGATCTTC
 GGTGTATCTCTTTGCTATTATTGAAAAAAGG

PRETTY of: /biotmp/msa118688.2{*} April 9, 2003 02:55 ..

	1				50
msa118688.2{361_18RS21}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_A909}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_COH1}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_H36B}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_JM9130013}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_M732}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{GBS361_2603}	atgagcgtat	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_090}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_1169NT}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_CJB110}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
msa118688.2{361_M781}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTTCTT	TGGGAAAGAA
Consensus	*****	*****	*****	*****	*****
	51				100
msa118688.2{361_18RS21}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAGAA	GGAATTTCTA
msa118688.2{361_A909}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAGAA	GGAATTTCTA
msa118688.2{361_COH1}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAGAA	GGAATTTCTA
msa118688.2{361_H36B}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAGAA	GGAATTTCTA
msa118688.2{361_JM9130013}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAGAA	GGAATTTCTA
msa118688.2{361_M732}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAGAA	GGAATTTCTA
msa118688.2{GBS361_2603}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAGAA	GGAATTTCTA
msa118688.2{361_090}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAGAA	GGAATTTCTA
msa118688.2{361_1169NT}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAGAA	GGAATTTCTA
msa118688.2{361_CJB110}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAGAA	GGAATTTCTA
msa118688.2{361_M781}	TTATAGCGAG	CATAAACAGC	ATCTCTTCGA	CTTAAAGAA	GGAATTTCTA
Consensus	*****	*****	*****	*****	*****
	101				150
msa118688.2{361_18RS21}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_A909}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_COH1}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_H36B}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_JM9130013}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_M732}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{GBS361_2603}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_090}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_1169NT}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_CJB110}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
msa118688.2{361_M781}	AACATTTATA	TAAAAATCAC	GACTCTATTT	TAGAATCTTA	TACAGGAAGC
Consensus	*****	*****	*****	*****	*****
	151				200
msa118688.2{361_18RS21}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_A909}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_COH1}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_H36B}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_JM9130013}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_M732}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{GBS361_2603}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_090}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_1169NT}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_CJB110}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
msa118688.2{361_M781}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTAA
Consensus	*****	*****	*****	*****	*****
	201				250
msa118688.2{361_18RS21}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msa118688.2{361_A909}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msa118688.2{361_COH1}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msa118688.2{361_H36B}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msa118688.2{361_JM9130013}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msa118688.2{361_M732}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msa118688.2{GBS361_2603}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msa118688.2{361_090}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msa118688.2{361_1169NT}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msa118688.2{361_CJB110}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
msa118688.2{361_M781}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCCTCAGGTG
Consensus	*****	*****	*****	*****	*****

Table 75: Comparative Sequences relating to SAG0671

	251		300
msa118688.2{361_18RS21}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_A909}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_COH1}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_H36B}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_JM9130013}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_M732}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{GBS361_2603}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_090}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_1169NT}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_CJB110}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
msa118688.2{361_M781}	TTAATTTAAA AGCTTATCAT	AATATTGCTG	TGTGTTTAGG GACCTCACTT
Consensus	*****	*****	*****
msa118688.2{361_18RS21}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_A909}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_COH1}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_H36B}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_JM9130013}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_M732}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{GBS361_2603}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_090}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_1169NT}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_CJB110}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
msa118688.2{361_M781}	GGGGGAAAGA GTGCTGGTCA	AAATGCCTTG	TATCAATTTG AAGAAGGAGA
Consensus	*****	*****	*****
msa118688.2{361_18RS21}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_A909}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_COH1}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_H36B}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_JM9130013}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_M732}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{GBS361_2603}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_090}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_1169NT}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_CJB110}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
msa118688.2{361_M781}	GCGTCAAGTA GATGCTAGTT	TATTAGAAAA	AGCATCTGTT TACCATATTG
Consensus	*****	*****	*****
msa118688.2{361_18RS21}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_A909}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_COH1}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_H36B}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_JM9130013}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_M732}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{GBS361_2603}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_090}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_1169NT}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_CJB110}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
msa118688.2{361_M781}	CTGATGAATT GATGGCTTAT	CATGATATTG	TGGGAGCTTC GTATGTTATT
Consensus	*****	*****	*****
msa118688.2{361_18RS21}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_A909}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_COH1}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_H36B}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_JM9130013}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_M732}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{GBS361_2603}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_090}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_1169NT}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_CJB110}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
msa118688.2{361_M781}	TCAACCGCCT GTTCTGCAAG	TAATAATGCC	GTAATATTAG GAACACAATT
Consensus	*****	*****	*****
msa118688.2{361_18RS21}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_A909}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_COH1}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_H36B}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_JM9130013}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_M732}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{GBS361_2603}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_090}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_1169NT}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_CJB110}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
msa118688.2{361_M781}	ACTTCAAGAT GGCATTGTG	ATTTAGCTAT	TTGTGGTGGC TGTGATGAGT
Consensus	*****	*****	*****

Table 75: Comparative Sequences relating to SAG0671

Consensus	*****	*****	*****	*****	*****
	551				600
msa118688.2{361_18RS21}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_A909}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_COH1}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_H36B}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_JM9130013}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_M732}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{GBS361_2603}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_090}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_1169NT}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_CJB110}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_M781}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
Consensus	*****	*****	*****	*****	*****
	601				650
msa118688.2{361_18RS21}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_A909}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_COH1}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_H36B}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_JM9130013}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_M732}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{GBS361_2603}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_090}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_1169NT}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_CJB110}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_M781}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
Consensus	*****	*****	*****	*****	*****
	651				700
msa118688.2{361_18RS21}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_A909}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_COH1}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_H36B}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_JM9130013}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_M732}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{GBS361_2603}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_090}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_1169NT}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_CJB110}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_M781}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
Consensus	*****	*****	*****	*****	*****
	701				750
msa118688.2{361_18RS21}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_A909}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_COH1}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_H36B}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_JM9130013}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_M732}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{GBS361_2603}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_090}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_1169NT}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_CJB110}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_M781}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
Consensus	*****	*****	*****	*****	*****
	751				800
msa118688.2{361_18RS21}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_A909}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_COH1}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_H36B}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_JM9130013}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_M732}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{GBS361_2603}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_090}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_1169NT}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_CJB110}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_M781}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
Consensus	*****	*****	*****	*****	*****
	801				850
msa118688.2{361_18RS21}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_A909}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_COH1}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_H36B}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_JM9130013}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_M732}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{GBS361_2603}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_090}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_1169NT}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA
msa118688.2{361_CJB110}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAc	GGTCACGGTA

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_M781}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAT	GGTCACGGTA
Consensus	*****	*****	*****	*****	*****
	851				900
msa118688.2{361_18RS21}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_A909}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_COH1}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_H36B}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_JM9130013}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_M732}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{GBS361_2603}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_090}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_1169NT}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_CJB110}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_M781}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
Consensus	*****	*****	*****	*****	*****
	901				950
msa118688.2{361_18RS21}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_A909}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_COH1}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_H36B}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_JM9130013}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_M732}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{GBS361_2603}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_090}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_1169NT}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_CJB110}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_M781}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
Consensus	*****	*****	*****	*****	*****
	951				1000
msa118688.2{361_18RS21}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_A909}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_COH1}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_H36B}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_JM9130013}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_M732}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{GBS361_2603}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_090}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_1169NT}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_CJB110}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_M781}	TCTAGGGGCT	GCAGGTATTA	TCGAATTGAT	TAATTGTTTA	GCGGCAATAG
Consensus	*****	*****	*****	*****	*****
	1001				1050
msa118688.2{361_18RS21}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_A909}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_COH1}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_H36B}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_JM9130013}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_M732}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{GBS361_2603}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_090}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_1169NT}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_CJB110}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_M781}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
Consensus	*****	*****	*****	*****	*****
	1051				1100
msa118688.2{361_18RS21}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_A909}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_COH1}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_H36B}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_JM9130013}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_M732}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{GBS361_2603}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_090}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_1169NT}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_CJB110}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_M781}	CCAGAAAAAT	TTGTCTATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
Consensus	*****	*****	*****	*****	*****
	1101				1150
msa118688.2{361_18RS21}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTTG
msa118688.2{361_A909}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTTG
msa118688.2{361_COH1}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTTG
msa118688.2{361_H36B}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTTG
msa118688.2{361_JM9130013}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTTG
msa118688.2{361_M732}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTTG
msa118688.2{GBS361_2603}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTTG
msa118688.2{361_090}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTTG
msa118688.2{361_1169NT}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTTG
msa118688.2{361_M781}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTTG
Consensus	*****	*****	*****	*****	*****

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_CJB110}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	aTCTTATTGT		
msa118688.2{361_M781}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	aTCTTATTGT		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1151	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA	1200
msa118688.2{361_A909}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_COH1}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_H36B}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_JM9130013}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_M732}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{GBS361_2603}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_090}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_1169NT}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_CJB110}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
msa118688.2{361_M781}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1201	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC	1250
msa118688.2{361_A909}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_COH1}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_H36B}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_JM9130013}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_M732}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{GBS361_2603}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_090}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_1169NT}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_CJB110}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
msa118688.2{361_M781}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1251	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC	1300
msa118688.2{361_A909}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_COH1}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_H36B}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_JM9130013}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_M732}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{GBS361_2603}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_090}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_1169NT}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_CJB110}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
msa118688.2{361_M781}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1301	GCTTTAAAGG	GGCTAGACCA	CCCAAAACTG	TCAACCCAGC	ACAATTTAGG	1350
msa118688.2{361_A909}	GCTTTAAAGG	GGCTAGACCA	CCCAAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_COH1}	GCTTTAAAGG	GGCTAGACCA	CCCAAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_H36B}	GCTTTAAAGG	GGCTAGACCA	CCCAAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_JM9130013}	GCTTTAAAGG	GGCTAGACCA	CCCAAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_M732}	GCTTTAAAGG	GGCTAGACCA	CCCAAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{GBS361_2603}	GCTTTAAAGG	GGCTAGACCA	CCCAAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_090}	GCTTTAAAGG	GGCTAGACCA	CCCAAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_1169NT}	GCTTTAAAGG	GGCTAGACCA	CCCAAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_CJB110}	GCTTTAAAGG	GGCTAGACCA	CCCAAAACTG	TCAACCCAGC	ACAATTTAGG		
msa118688.2{361_M781}	GCTTTAAAGG	GGCTAGACCA	CCCAAAACTG	TCAACCCAGC	ACAATTTAGG		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1351	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT	1400
msa118688.2{361_A909}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_COH1}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_H36B}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_JM9130013}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_M732}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{GBS361_2603}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_090}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_1169NT}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_CJB110}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
msa118688.2{361_M781}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT		
Consensus	*****	*****	*****	*****	*****		
msa118688.2{361_18RS21}	1401	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA	1450
msa118688.2{361_A909}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA		
msa118688.2{361_COH1}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA		
msa118688.2{361_H36B}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA		
msa118688.2{361_JM9130013}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA		
msa118688.2{361_M732}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA		
msa118688.2{GBS361_2603}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA		
msa118688.2{361_090}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA		

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_1169NT}	AATAGAAAGC	AATATTAATC	TAAAAAAACA	AGATACTTCA	AAAGTAGGAA	
msa118688.2{361_CJB110}	AATAGAAAGC	AATATTAATC	TAAAAAAACA	AGATACTTCA	AAAGTAGGAA	
msa118688.2{361_M781}	AATAGAAAGC	AATATTAATC	TAAAAAAACA	AGATACTTCA	AAAGTAGGAA	
Consensus	*****	*****	*****	*****	*****	
msa118688.2{361_18RS21}	1451	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
msa118688.2{361_A909}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA	
msa118688.2{361_COH1}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA	
msa118688.2{361_H36B}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA	
msa118688.2{361_JM9130013}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA	
msa118688.2{361_M732}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA	
msa118688.2{GBS361_2603}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA	
msa118688.2{361_090}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA	
msa118688.2{361_1169NT}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA	
msa118688.2{361_CJB110}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA	
msa118688.2{361_M781}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA	
Consensus	*****	*****	*****	*****	*****	
msa118688.2{361_18RS21}	1501	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC
msa118688.2{361_A909}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC	
msa118688.2{361_COH1}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC	
msa118688.2{361_H36B}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC	
msa118688.2{361_JM9130013}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC	
msa118688.2{361_M732}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC	
msa118688.2{GBS361_2603}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC	
msa118688.2{361_090}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC	
msa118688.2{361_1169NT}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC	
msa118688.2{361_CJB110}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC	
msa118688.2{361_M781}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC	
Consensus	*****	*****	*****	*****	*****	
msa118688.2{361_18RS21}	1551	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA
msa118688.2{361_A909}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA	
msa118688.2{361_COH1}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA	
msa118688.2{361_H36B}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA	
msa118688.2{361_JM9130013}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA	
msa118688.2{361_M732}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA	
msa118688.2{GBS361_2603}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA	
msa118688.2{361_090}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA	
msa118688.2{361_1169NT}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA	
msa118688.2{361_CJB110}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA	
msa118688.2{361_M781}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAAA	
Consensus	*****	*****	*****	*****	*****	
msa118688.2{361_18RS21}	1601	TAACAGGTCC	TTTATCTGTC	ATTTCGACAA	ATAGTGGAGC	GCTTGATGGT
msa118688.2{361_A909}	TAACAGGTCC	TTTATCTGTC	ATTTCGACAA	ATAGTGGAGC	GCTTGATGGT	
msa118688.2{361_COH1}	TAACAGGTCC	TTTATCTGTC	ATTTCGACAA	ATAGTGGAGC	GCTTGATGGT	
msa118688.2{361_H36B}	TAACAGGTCC	TTTATCTGTC	ATTTCGACAA	ATAGTGGAGC	GCTTGATGGT	
msa118688.2{361_JM9130013}	TAACAGGTCC	TTTATCTGTC	ATTTCGACAA	ATAGTGGAGC	GCTTGATGGT	
msa118688.2{361_M732}	TAACAGGTCC	TTTATCTGTC	ATTTCGACAA	ATAGTGGAGC	GCTTGATGGT	
msa118688.2{GBS361_2603}	TAACAGGTCC	TTTATCTGTC	ATTTCGACAA	ATAGTGGAGC	GCTTGATGGT	
msa118688.2{361_090}	TAACAGGTCC	TTTATCTGTC	ATTTCGACAA	ATAGTGGAGC	GCTTGATGGT	
msa118688.2{361_1169NT}	TAACAGGTCC	TTTATCTGTC	ATTTCGACAA	ATAGTGGAGC	GCTTGATGGT	
msa118688.2{361_CJB110}	TAACAGGTCC	TTTATCTGTC	ATTTCGACAA	ATAGTGGAGC	GCTTGATGGT	
msa118688.2{361_M781}	TAACAGGTCC	TTTATCTGTC	ATTTCGACAA	ATAGTGGAGC	GCTTGATGGT	
Consensus	*****	*****	*****	*****	*****	
msa118688.2{361_18RS21}	1651	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
msa118688.2{361_A909}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT	
msa118688.2{361_COH1}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT	
msa118688.2{361_H36B}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT	
msa118688.2{361_JM9130013}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT	
msa118688.2{361_M732}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT	
msa118688.2{GBS361_2603}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT	
msa118688.2{361_090}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT	
msa118688.2{361_1169NT}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT	
msa118688.2{361_CJB110}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT	
msa118688.2{361_M781}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT	
Consensus	*****	*****	*****	*****	*****	
msa118688.2{361_18RS21}	1701	TCTTGTTCCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC
msa118688.2{361_A909}	TCTTGTTCCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC	
msa118688.2{361_COH1}	TCTTGTTCCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC	
msa118688.2{361_H36B}	TCTTGTTCCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC	
msa118688.2{361_JM9130013}	TCTTGTTCCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC	
msa118688.2{361_M732}	TCTTGTTCCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC	
msa118688.2{GBS361_2603}	TCTTGTTCCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC	

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_090}	TCTTGTTCCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC
msa118688.2{361_1169NT}	TCTTGTTCCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC
msa118688.2{361_CJB110}	TCTTGTTCCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC
msa118688.2{361_M781}	TCTTGTTCCT	GCTAATCAGT	GGACAGACAT	GAGTTTATG	TGGTGGCAAC
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	1751 AATTAACTA	TGATAGTCAA	ATGTTTGTTCG	GTTCTGATTA	1800 TTGTTTCAGCA
msa118688.2{361_A909}	AATTAACTA	TGATAGTCAA	ATGTTTGTTCG	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_COH1}	AATTAACTA	TGATAGTCAA	ATGTTTGTTCG	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_H36B}	AATTAACTA	TGATAGTCAA	ATGTTTGTTCG	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_JM9130013}	AATTAACTA	TGATAGTCAA	ATGTTTGTTCG	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_M732}	AATTAACTA	TGATAGTCAA	ATGTTTGTTCG	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{GBS361_2603}	AATTAACTA	TGATAGTCAA	ATGTTTGTTCG	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_090}	AATTAACTA	TGATAGTCAA	ATGTTTGTTCG	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_1169NT}	AATTAACTA	TGATAGTCAA	ATGTTTGTTCG	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_CJB110}	AATTAACTA	TGATAGTCAA	ATGTTTGTTCG	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_M781}	AATTAACTA	TGATAGTCAA	ATGTTTGTTCG	GTTCTGATTA	TTGTTTCAGCA
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	1801 CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	1850 TATTAGGTAG
msa118688.2{361_A909}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_COH1}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_H36B}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_JM9130013}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_M732}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{GBS361_2603}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_090}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_1169NT}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_CJB110}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_M781}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	1851 TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	1900 ATGACTATTT
msa118688.2{361_A909}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_COH1}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_H36B}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_JM9130013}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_M732}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{GBS361_2603}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_090}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_1169NT}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_CJB110}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_M781}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	1901 TTGATGCTGC	GCITCAAAT	TTATTATCAG	ACTTAGGACT	1950 AACCATAAAA
msa118688.2{361_A909}	TTGATGCTGC	GCITCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_COH1}	TTGATGCTGC	GCITCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_H36B}	TTGATGCTGC	GCITCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_JM9130013}	TTGATGCTGC	GCITCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_M732}	TTGATGCTGC	GCITCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{GBS361_2603}	TTGATGCTGC	GCITCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_090}	TTGATGCTGC	GCITCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_1169NT}	TTGATGCTGC	GCITCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_CJB110}	TTGATGCTGC	GCITCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_M781}	TTGATGCTGC	GCITCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	1951 GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	2000 TTAGTTCAGA
msa118688.2{361_A909}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_COH1}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_H36B}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_JM9130013}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_M732}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{GBS361_2603}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_090}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_1169NT}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_CJB110}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_M781}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
Consensus	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	2001 TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	2050 CCAAACCTTG
msa118688.2{361_A909}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_COH1}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_H36B}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_JM9130013}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_M732}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{GBS361_2603}	TTATGATTTC	TTAGCGAACT	TGCTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_090}	TTATGATTTC	TTAGCGAACT	TGCTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_1169NT}	TTATGATTTC	TTAGCGAACT	TGCTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_CJB110}	TTATGATTTC	TTAGCGAACT	TGCTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_M781}	TTATGATTTC	TTAGCGAACT	TGCTCTGAGTA	TTATAATATG	CCAAACCTTG
Consensus	*****	*****	*****	*****	*****
2051					2100
msa118688.2{361_18RS21}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_A909}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_COH1}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_H36B}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_JM9130013}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_M732}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{GBS361_2603}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_090}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_1169NT}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_CJB110}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
msa118688.2{361_M781}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAACTGGAC
Consensus	*****	*****	*****	*****	*****
2101					2150
msa118688.2{361_18RS21}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_A909}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_COH1}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_H36B}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_JM9130013}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_M732}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{GBS361_2603}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_090}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_1169NT}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_CJB110}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_M781}	TATACTGTGA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
Consensus	*****	*****	*****	*****	*****
2151					2193
msa118688.2{361_18RS21}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_A909}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_COH1}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_H36B}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_JM9130013}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_M732}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{GBS361_2603}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_090}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_1169NT}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_CJB110}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_M781}	TTCGATCTTC	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
Consensus	*****	*****	*****	*****	***

SEQ ID NO. 7512

STRAIN 2603 frame: 1

MSVYVSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESITSDPEVPEQ
 YKDETRNFKAFAFEALASSGVNLKAYHNIACVCLGTSLGKKSAGQNALYQFEEGERQV
 DASLLEKASVYHIADELMAYHDI VGASYVISTACASANNVILGTQLLDQDCLDAICGG
 CDELSDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYKGIIGGL
 ITSDGYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKF
 FPTTLISSTKGQTGHTLGAAGIIELINCLAAIEEQVTPATKNEIGIEGFENFVYHQKR
 EYPRNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITY
 EKVASNFNDFEALRFKGRPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTS
 KVGIVFTTSLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSV
 ISTNSGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWQQNLNYSQMFVGS DYCSA
 QVLSRQALDNPILGSKQLKYSKHTFTDVTI FDAALQNLSDGLTI IKDIGFVWNER
 KKA VSSDYDFLANLSEYNNMPLNASGQFGFSSNGAGEELDYTVNESIEKGYLVLSYSIF
 GGISFAIIEKR

SEQ ID NO. 7513

STRAIN 090 frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESITSDPEVPEQYKDE
 TRNFKAFAFEALASSGVNLKAYHNIACVCLGTSLGKKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACASANNVILGTQLLDQDCLDAICGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYKGIIGGLITSD
 GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFPTT
 TLISSTKGQTGHTLGAAGIIELINCLAAIEEQVTPATKNEIGIEGFENFVYHQKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYE
 KVA SNFNDFEALRFKGRPPKTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSK
 VGI VFTTSLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVI
 STNSGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWQQNLNYSQMFVGS DYCSA
 QVLSRQALDNPILGSKQLKYSKHTFTDVTI FDAALQNLSDGLTI IKDIGFVWNERKKA
 VSSDYDFLANLSEYNNMPLNASGQFGFSSNGAGEELDYTVNESIEKGYLVLSYSIFGGIS
 FAIIEKR

SEQ ID NO. 7514

STRAIN A909 frame: 3

Table 75: Comparative Sequences relating to SAG0671

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTSLGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACASNNAVILGTQLLQDGDCLAI CGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKI IGG LITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSSTKGQTGHTLGAAGII ELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGPAPKPTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNLLSDLG LTI KD IKGFWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVSYISFGGIS
 FAIIEKR

SEQ ID NO. 7515

STRAIN H36B frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTSLGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACASNNAVILGTQLLQDGDCLAI CGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKI IGG LITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSSTKGQTGHTLGAAGII ELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGPAPKPTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNLLSDLG LTI KD IKGFWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVSYISFGGIS
 FAIIEKR

SEQ ID NO. 7516

STRAIN 18RS21 frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTSLGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACASNNAVILGTQLLQDGDCLAI CGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKI IGG LITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSSTKGQTGHTLGAAGII ELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGPAPKPTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNLLSDLG LTI KD IKGFWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVSYISFGGIS
 FAIIEKR

SEQ ID NO. 7517

STRAIN M732 frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTSLGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACASNNAVILGTQLLQDGDCLAI CGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKI IGG LITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSSTKGQTGHTLGAAGII ELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGPAPKPTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNLLSDLG LTI KD IKGFWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVSYISFGGIS
 FAIIEKR

SEQ ID NO. 7518

STRAIN COH1 frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTSLGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDI VGASYVISTACASNNAVILGTQLLQDGDCLAI CGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKI IGG LITSD
 GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
 TLISSSTKGQTGHTLGAAGII ELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI
 RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGPAPKPTVNPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS
 RQALDNSPI ILGSKQLKYSHKTFDVTI FDAALQNLLSDLG LTI KD IKGFWNERKKAV
 SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVSYISFGGIS
 FAIIEKR

SEQ ID NO. 7519

STRAIN M781 frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNI AVCLGTSLGGKSAGQNALYQFEEGERQVDASL

Table 75: Comparative Sequences relating to SAG0671

LEKASVYHIADELMAYHDI VGASYVISTACASANNVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQVTPATKNEIGIEGFPENFVYHQREYPI
RNALNFSFAFGGNNSSGILLSSLDSPLETLPAENLKMALSSVASISKNESLSITYEKVA
SNFNDFEALRFKARGPPKTVNPAQFRKMDDFSKMVAVTTAQAALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGSYCSAQVLS
RQALDNPFIILGSKQLKYSHKTFDVTMTIFDAALQNLSDGLGTIKDIGFVWNERKKA
SSDYDFLANLSEYNNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYVLVLSYSIFGGIS
FAIEKR

SEQ ID NO. 7520

STRAIN CJB110 frame: 3

VSGIGIISLGGKNYSEHKQHLFDLKEGISKHLYKNHDSILESITSGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIACVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDI VGASYVISTACASANNVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQVTPATKNEIGIEGFPENFVYHQREYPI
RNALNFSFAFGGNNSSGILLSSLDSPLETLPAENLKMALSSVASISKNESLSITYEKVA
SNFNDFEALRFKARGPPKTVNPAQFRKMDDFSKMVAVTTAQAALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGSYCSAQVLS
RQALDNPFIILGSKQLKYSHKTFDVTMTIFDAALQNLSDGLGTIKDIGFVWNERKKA
SSDYDFLANLSEYNNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYVLVLSYSIFGGIS
FAIEKR

SEQ ID NO. 7521

STRAIN 1169NT frame: 3

VSGIGIISLGGKNYSEHKQHLFDLKEGISKHLYKNHDSILESITSGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIACVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDI VGASYVISTACASANNVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQVTPATKNEIGIEGFPENFVYHQREYPI
RNALNFSFAFGGNNSSGILLSSLDSPLETLPAENLKMALSSVASISKNESLSITYEKVA
SNFNDFEALRFKARGPPKTVNPAQFRKMDDFSKMVAVTTAQAALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGSYCSAQVLS
RQALDNPFIILGSKQLKYSHKTFDVTMTIFDAALQNLSDGLGTIKDIGFVWNERKKA
SSDYDFLANLSEYNNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYVLVLSYSIFGGIS
FAIEKR

SEQ ID NO. 7522

STRAIN JM9130013 frame: 3

VSGIGIISLGGKNYSEHKQHLFDLKEGISKHLYKNHDSILESITSGSITSDPEVPEQYKDE
TRNFKFAFTAFEEALASSGVNLKAYHNIACVCLGTSLGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDI VGASYVISTACASANNVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKIIGGLITSD
GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQVTPATKNEIGIEGFPENFVYHQREYPI
RNALNFSFAFGGNNSSGILLSSLDSPLETLPAENLKMALSSVASISKNESLSITYEKVA
SNFNDFEALRFKARGPPKTVNPAQFRKMDDFSKMVAVTTAQAALIESNINLKKQDTSKVGI
VFTTLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGSYCSAQVLS
RQALDNPFIILGSKQLKYSHKTFDVTMTIFDAALQNLSDGLGTIKDIGFVWNERKKA
SSDYDFLANLSEYNNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYVLVLSYSIFGGIS
FAIEKR

PRETTY of: /biotmp/msa118713.2{*} April 9, 2003 02:54 ..

	1	50
msa118713.2{361_090}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESITGS
msa118713.2{361_1169NT}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESITGS
msa118713.2{361_CJB110}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESITGS
msa118713.2{361_M781}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESITGS
msa118713.2{361_18RS21}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESITGS
msa118713.2{361_A909}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESITGS
msa118713.2{361_COH1}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESITGS
msa118713.2{361_H36B}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESITGS
msa118713.2{361_JM9130013}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESITGS
msa118713.2{361_M732}	----VSGIGI	ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESITGS
msa118713.2{GBS361_2603}	msvYVSGIGI	ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESITGS
Consensus	*****	*****
	51	100
msa118713.2{361_090}	ITSDPEVPEQ	YKDETRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTSL
msa118713.2{361_1169NT}	ITSDPEVPEQ	YKDETRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTSL
msa118713.2{361_CJB110}	ITSDPEVPEQ	YKDETRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTSL
msa118713.2{361_M781}	ITSDPEVPEQ	YKDETRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTSL
msa118713.2{361_18RS21}	ITSDPEVPEQ	YKDETRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTSL

Table 75: Comparative Sequences relating to SAG0671

msa118713.2{361_A909}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{361_COH1}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{361_H36B}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{361_JM9130013}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{361_M732}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{GBS361_2603}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_1169NT}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_CJB110}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_M781}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_18RS21}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_A909}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_COH1}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_H36B}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_JM9130013}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_M732}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{GBS361_2603}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_1169NT}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_CJB110}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_M781}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_18RS21}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_A909}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_COH1}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_H36B}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_JM9130013}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{361_M732}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
msa118713.2{GBS361_2603}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAINT
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_1169NT}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_CJB110}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_M781}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_18RS21}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_A909}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_COH1}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_H36B}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_JM9130013}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_M732}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{GBS361_2603}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_1169NT}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_CJB110}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_M781}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_18RS21}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_A909}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_COH1}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_H36B}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_JM9130013}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_M732}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{GBS361_2603}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	FPTTTLISST	KGQTGHTLGA	AGIIE LINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_1169NT}	FPTTTLISST	KGQTGHTLGA	AGIIE LINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_CJB110}	FPTTTLISST	KGQTGHTLGA	AGIIE LINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_M781}	FPTTTLISST	KGQTGHTLGA	AGIIE LINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_18RS21}	FPTTTLISST	KGQTGHTLGA	AGIIE LINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_A909}	FPTTTLISST	KGQTGHTLGA	AGIIE LINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_COH1}	FPTTTLISST	KGQTGHTLGA	AGIIE LINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_H36B}	FPTTTLISST	KGQTGHTLGA	AGIIE LINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_JM9130013}	FPTTTLISST	KGQTGHTLGA	AGIIE LINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_M732}	FPTTTLISST	KGQTGHTLGA	AGIIE LINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{GBS361_2603}	FPTTTLISST	KGQTGHTLGA	AGIIE LINCL	AAIEBQTVPA	TKNEIGIEGF
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	PENFVYHQKR	EYPIRNALNF	SFAPGGNSG	ILLSSLDSP	ETLPARENLK
msa118713.2{361_1169NT}	PENFVYHQKR	EYPIRNALNF	SFAPGGNSG	ILLSSLDSP	ETLPARENLK
msa118713.2{361_CJB110}	PENFVYHQKR	EYPIRNALNF	SFAPGGNSG	ILLSSLDSP	ETLPARENLK
msa118713.2{361_M781}	PENFVYHQKR	EYPIRNALNF	SFAPGGNSG	ILLSSLDSP	ETLPARENLK

Table 75: Comparative Sequences relating to SAG0671

msa118713.2{361_18RS21}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK
msa118713.2{361_A909}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK
msa118713.2{361_COH1}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK
msa118713.2{361_H36B}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK
msa118713.2{361_JM9130013}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK
msa118713.2{361_M732}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK
msa118713.2{GBS361_2603}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK
Consensus	*****	*****	*****	*****	*****
401					
msa118713.2{361_090}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGAR	PKTVNPAQFR
msa118713.2{361_1169NT}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGAR	PKTVNPAQFR
msa118713.2{361_CJB110}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGAR	PKTVNPAQFR
msa118713.2{361_M781}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGAR	PKTVNPAQFR
msa118713.2{361_18RS21}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGAR	PKTVNPAQFR
msa118713.2{361_A909}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGAR	PKTVNPAQFR
msa118713.2{361_COH1}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGAR	PKTVNPAQFR
msa118713.2{361_H36B}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGAR	PKTVNPAQFR
msa118713.2{361_JM9130013}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGAR	PKTVNPAQFR
msa118713.2{361_M732}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGAR	PKTVNPAQFR
msa118713.2{GBS361_2603}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGAR	PKTVNPAQFR
Consensus	*****	*****	*****	*****	*****
451					
msa118713.2{361_090}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_1169NT}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_CJB110}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_M781}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_18RS21}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_A909}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_COH1}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_H36B}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_JM9130013}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_M732}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{GBS361_2603}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
Consensus	*****	*****	*****	*****	*****
501					
msa118713.2{361_090}	KQITTEGYAH	VSASRFPPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_1169NT}	KQITTEGYAH	VSASRFPPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_CJB110}	KQITTEGYAH	VSASRFPPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_M781}	KQITTEGYAH	VSASRFPPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_18RS21}	KQITTEGYAH	VSASRFPPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_A909}	KQITTEGYAH	VSASRFPPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_COH1}	KQITTEGYAH	VSASRFPPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_H36B}	KQITTEGYAH	VSASRFPPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_JM9130013}	KQITTEGYAH	VSASRFPPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_M732}	KQITTEGYAH	VSASRFPPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{GBS361_2603}	KQITTEGYAH	VSASRFPPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
Consensus	*****	*****	*****	*****	*****
551					
msa118713.2{361_090}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA
msa118713.2{361_1169NT}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA
msa118713.2{361_CJB110}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA
msa118713.2{361_M781}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA
msa118713.2{361_18RS21}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA
msa118713.2{361_A909}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA
msa118713.2{361_COH1}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA
msa118713.2{361_H36B}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA
msa118713.2{361_JM9130013}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA
msa118713.2{361_M732}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA
msa118713.2{GBS361_2603}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGS DYCSA
Consensus	*****	*****	*****	*****	*****
601					
msa118713.2{361_090}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_1169NT}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_CJB110}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_M781}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_18RS21}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_A909}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_COH1}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_H36B}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_JM9130013}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_M732}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{GBS361_2603}	QVLSRQALDN	SPIILGSKQL	KYSHKTFITDV	MTIFDAALQN	LLSDLGLTIK
Consensus	*****	*****	*****	*****	*****
651					
msa118713.2{361_090}	DIKGFVWNER	KKAVSSDYDF	LANLSEYNYM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_1169NT}	DIKGFVWNER	KKAVSSDYDF	LANLSEYNYM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_CJB110}	DIKGFVWNER	KKAVSSDYDF	LANLSEYNYM	PNLASGQFGF	SSNGAGEELD

Table 75: Comparative Sequences relating to SAG0671

msa118713.2{361_M781}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_18RS21}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_A909}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_COH1}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_H36B}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_JM9130013}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_M732}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{GBS361_2603}	DIKGFVWNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
Consensus	*****	*****	*****	*****	*****
	701			731	
msa118713.2{361_090}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_1169NT}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_CJB110}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_M781}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_18RS21}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_A909}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_COH1}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_H36B}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_JM9130013}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{361_M732}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
msa118713.2{GBS361_2603}	YTVNESIEKG	YYLVLSYSIF	GGISFAIEK	R	
Consensus	*****	*****	*****	*	

Table 76: Comparative Sequences relating to SAG0260

SEQ ID NO. 7601

STRAIN 2603

ATGAAAAAAGTCATCGATTAAAAAACTACAAAAAGCATATGCCTCAGAAACCGTTTAA
 AATAATATTAAATTGGAGGTGTTTAAAGGCGAAATAATTGGATTAAATAGGACCCCTCTGGA
 GCAGGGAATCTACCTTGATTAAAACTATGCTTGGCATGAAAAAGCAGATAAGGGAACA
 GCTCTTGTCTTGATACCTCAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATG
 GCTCAATCTGATGCCCTTATACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCTTTGGA
 AAAATGAAAGGTATTCAAAAACTGAATTAACACAGCAGATAACTCATATTTCTAAAGTA
 GTAGATCTAGAAAACCAACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGAAAAGA
 CGGCTTTCTAGCCATCGCCCTACTTGGAAACCCACAGTTTAACTCCTAGATGAACCT
 ACCGTTGGAATTGATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAG
 GATGAAGACATTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAATTAACAAGT
 AAGGTGCACTACTATTACGTGGAACATTATTGCCCTTGATACTCCATTACATTTAAAA
 AAACAATTTAATGTGAGTACTATTGAGGAAGTTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7602

STRAIN 090

ATTTAAAAAACTACAAAAAGCATATGCCTCAGAAACTGTTTTAAATAAT
 ATTAATTTGGAGGTGTTTAAAGGCGAAATAATTGGATTAAATAGGACCCCTC
 TGGAGCAGGGAATCTACCTTGATTAAAACTATGCTTGGCATGAAAAAG
 CAGATAAGGGAACAGCTCTTGTCTTGATACTCAAATGCCAGATCGTAAT
 ATTTTAAATCAAATTGGCTATATGGCTCAATCTGATGCCCTTATACGAATC
 TTTAACTGCCCTTAGAAATTTATTATTCTTTGGAAAAATGAAAGGTATTCT
 AAAAACTGAATTAAAAACAGCAGATAACTCATATTTCTAAAGTAGTAGAT
 CTAGAAAACCAACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGAA
 AAGACGGCTTTCTAGCCATCGCCCTACTTGGAAACCCACAGTTTAA
 TCCTAGATGAACCTACCGTTGGAATTGATCCATCCTTGAGGAGAAAAATC
 TGGCAAGAGCTAATTAATATTAAAGGATGAAGGACGTTCTATCTTTATTAC
 AACCCACCTTATGGATGAAGCAGAAATTAACAAGTAAGGTTGCACTACTAT
 TACGTGGAACATTATTGCCCTTGATACTCCATTACATTTAAAAAAACAA
 TTTAATGTGAGTACTATTGAGGAAGTTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7603

STRAIN A909

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATATGCCTCA
 GAAACCGTTTTAAATAATATTAAATTTGGAGGTGTTTAAAGGCGAAATAAT
 TGGATTAAATAGGACCCCTCTGGAGCAGGGAATCTACCTTGATTAAAACTA
 TGCTTGGCATGAAAAAGCAGATAAGGGAACAGCTCTTGTCTTGATACT
 CAAATGCCAGATCATAATATTTTAAATCAAATTGGCTATATGGCTCAATC
 TGATGCCCTTATACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCTTTG
 GAAAAATGAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAACTCAT
 ATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTCAGG
 TTAATCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTACTTG
 GAAACCCACAGTTTTAATCTAGATGAACCTACCGTTGGAATTGATCCA
 TCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGATGAAGG
 ACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAATTAACAA
 GTAAGGTTGCACTACTATTACGTGGAACATTATTGCCCTTGATACTCCA
 TTACATTTAAAAAAACAAATTTAATGTGAGTACTATTGAGGAAGTTTTCTT
 AAAAGCTGAAGGAGAA

SEQ ID NO. 7604

STRAIN H36B

AAAAAAGTCATTGATTAAAAAACTACAAAAAGCATATGCC
 TCAGAAACCGTTTTAAATAATATTAAATTTGGAGGTGTTTAAAGGCGAAAT
 AATTGGATTAAATAGGACCCCTCTGGAGCAGGGAATCTACCTTGATTAAAA
 CTATGCTTGGCATGAAAAAGCAGATAAGGGAACAGCTCTTGTCTTGAT
 ACTCAAATGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCTCA
 ATCTGATGCCCTTATACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCT
 TTGAAAAATGAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAACT
 CATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTC
 AGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTAC
 TTGGAACCCACAGTTTTAATCTAGATGAACCTACCGTTGGAATTGAT
 CCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGATGA
 AGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAATTA
 CAAGTAAGGTTGCACTACTATTACGTGGAACATTATTGCCCTTGATACT
 CCATTACATTTAAAAAAACAAATTTAATGTGAGTACTATTGAGGAAGTTTT
 CTTAAAGCTGAAGGAGAA

SEQ ID NO. 7605

STRAIN 18RS21

GATTTAAAAAACTACAAAAAGCATATGCCTCAGAAACCGTTTTAAATAA
 TATTAAATTTGGAGGTGTTTAAAGGCGAAATAATTGGATTAAATAGGACCCCT
 CTGGAGCAGGGAATCTACCTTGATTAAAACTATGCTTGGCATGAAAAA
 GCAGATAAGGGAACAGCTCTTGTCTTGATACTCAAATGCCAGATCGTAA
 TATTTTAAATCAAATTGGCTATATGGCTCAATCTGATGCCCTTATACGAGT
 CTTTAACTGGCTTAGAAAAATTTATTATTCTTTGAAAAATGAAAGGTATT
 CAAAAACCTGAATTAAAAACAGCAGATAACTCATATTTCTAAAGTAGTAGA
 TCTAGAAAACCAACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGA
 AAGACGGCTTTCTCTAGCCATCGCCCTACTTGGAAACCCACAGTTTAA
 ATCCTAGATGAACCTACCGTTGGAATTGATCCATCCTTGAGGAGAAAAAT
 CTGGCAAGAGCTAATTAATATTAAAGGATGAAGGACATTTCTATCTTTATTA
 CAACCCACGTTATGGATGAAGCAGAAATTAACAAGTAAGGTTGCACTACTA

Table 76: Comparative Sequences relating to SAG0260

TTACGTGGAACATTATTGCCCTTGATACTCCATTACATTAAAAAACA
ATTTAATGTGAGTACTATTGAGGAAGTTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7606

STRAIN M732

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATACGCCTCA
GAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGAGAAATAAT
TGGATTAAATAGGACCCTCTGGAGCAGGGAATCTACCTTGATTAAAACTA
TGCTTGGCATGAAAAAGCAGATAAGGGAACAGCTCTTGTCTTGATACT
CAAATGCCAGATCGTAATTTTAAATCAAATTGGCTATATGGCTCAATC
TGATGCCCTTACACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCTTG
GAAAAATGAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAAATCAT
ATTTCTAAAGTAGTAGATCTAGAAAACCACTTGATAAATTTGTCTCAGG
TTACTCAGGAGGTATGAAAAGACGGCTTTCTTAGCCATCGCCCTACTTG
GAAACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTGATCCA
TCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGATGAAGG
ACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAAACA
GTAAGGTGCACTACTATTACGTGGAACATTATTGCCTTTGATACTCCA
TTACATTAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTTTCTT
AAAAGCTGAAGGAGAA

SEQ ID NO. 7607

STRAIN COH1

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATACGCCTCAGAA
ACITGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGAGAAATAATTGG
ATTAAATAGGACCCTCTGGAGCAGGGAATCTACCTTGATTAAAACTATGC
TTGGCATGGAATAAGCAGATAAGGGAACAGCTCTTGTCTTGATACTCAA
ATGCCAGATCGTAATTTTAAATCAAATTGGCTATATGGCTCAATCTGA
TGCTTTACACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCTTGGA
AAATGAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAAATCATATT
TCTAAAGTAGTAGATCTAGAAAACCACTTGATAAATTTGTCTCAGGTTA
TCTCAGGAGGTATGAAAAGACGGCTTTCTTAGCCATCGCCCTACTTGGA
ACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTGATCCATCC
TTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGATGAAGGACG
TTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTAAACAAGTA
AGGTTGCACTACTATTACGTGGAACATTATTGCCTTTGATACTCCATTA
CAITTTAAAAAACAATTTAATGTGAGTACTATTGAGGAAG

SEQ ID NO. 7608

STRAIN M781

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATAC
GCCTCAGAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGAGA
AATAATTGGATTAAATAGGACCCTCTGGAGCAGGGAATCTACCTTGATTAA
AACTATGCTTGGCATGGAATAAGCAGATAAGGGAACAGCTCTTGTCTCT
GATACTCAAATGCCAGATCGTAATTTTAAATCAAATTGGCTATATGGC
TCAATCTGATGCCCTTACACGAGTCTTTAACTGGCTTAGAAAAATTTATTAT
TCTTTGGAATAAGTAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATA
ACTCATATTTCTAAAGTAGTAGATCTAGAAAACCACTTGATAAATTTGT
CTCAGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTTAGCCATCGCCC
TACTTGGAACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATT
GATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGA
TGAAGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAT
TAACAAGTAAGGTTGCACTACTATTACGTGGAACATTATTGCCTTTGAT
ACTCCATTACATTAAAAAACAATTTAATGTGAGTACTATTGAGGAAGT
TTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7609

STRAIN CJB110

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATATG
CCTCAGAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGCGAA
ATAATTGGATTAAATAGGACCCTCTGGAGCAGGGAATCTACCTTGATTAA
AACTATGCTTGGCATGGAATAAGCAGATAAGGGAACAGCTCTTGTCTTG
ATACTCAAATGCCAGATCGTAATTTTAAATCAAATTGGCTATATGGCT
CAATCTGATGCCCTTATACGAATCTTTAACTGCTTAGAAAAATTTATTATT
CTTTGGAATAAGTAAAGGTATTCAAAAACTGAATTAAAAACAGCAGATAA
CTCATATTTCTAAAGTAGTAGATCTAGAAAACCACTTGATAAATTTGTC
TCAGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTTAGCCATCGCCCT
ACTTGGAACCCACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTG
ATCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAAGGAT
GAAGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAT
AACAAGTAAGGTTGCACTACTATTACGTGGAACATTATTGCCTTTGATA
CTCCATTACATTAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTT
TTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7610

STRAIN 1169NT

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATAC
GCCTCAGAAACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGCGA
AATAATTGGATTAAATAGGACCCTCTGGAGCAGGGAATCTACCTTGATTAA
AACTATGCTTGGCATGGAATAAGCAGATAAGGGAACAGCTCTTGTCTCT
GATACTCAAATGCCAGATCGTAATTTTAAATCAAATTGGCTATATGGC
TCAATCTGATGCCCTTATACGAATCTTTAACTGCTTAGAAAAATTTATTAT

Table 76: Comparative Sequences relating to SAG0260

TCTTTGGAAAAATGAAAAGGTATTCAAAAACTGAATTAACAGCAGATA
 ACTCATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAAATTTGT
 CTCAGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCC
 TACTTGGAAACCCACAGTTTAAATCCTAGATGAACCTACCGTTGGAATT
 GATCCATCCTTGAGGAGAAAATCTGGCAAGAGCTAATTAATATTAAAGGA
 TGAAGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAT
 TAACAAGTAAGGTTGCCTACTATTACGTGGAAACATTATTGCCTTTGAT
 ACTCCATTACATTTAAAAAAACAATTAATGTGAGTACTATTGAGGAAGT
 TTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7611

STRAIN JM9130013

AAAAAAGTCATCGATTTAAAAAACTACAAAAGCATATGCC
 TCAGAAACCGTTTAAATAATATTAAATTTGGAGGTGTTTAAAGGCGAAAT
 AATTTGGATTAATAGGACCTCTGGAGCAGGAAATCTACCTTGATTAAAA
 CTATGCTTGGCATGGAAAAGCAGATAAGGGAACAGCTCTTGTTCCTGAT
 ACTCAAATGCCAGATCGTAATATTTTAAATCAAATTTGGCTATATGGCTCA
 ATCTGATGCCCTTATACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCT
 TTGGAATAATGAAAGGTATTCAAAAACTGAATTAACAGCAGATAAAT
 CATATTTCTAAAGTAGTAGATCTAGAAAACCAACTTGATAAAATTTGTCTC
 AGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTAC
 TTGGAACCCACAGTTTAAATCCTAGATGAACCTACCGTTGGAATTGAT
 CCATCCTTGAGGAGAAAATCTGGCAAGAGCTAATTAATATTAAAGGATGA
 AGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTA
 CAAGTAAGGTTGCACTACTATTACGTGGAAACATTATTGCCTTTGATACT
 CCATTACATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTTT
 CTTAAAGCTGAAGGAGAA

PRETTY of: /biotmp/msa134270.2{*} April 10, 2003 02:14 ..

	1				50
msa134270.2{391_COH1}	-----aaaaaaag	tcacgcgATTT	AAAAAAACTA	CAAAAAGCAT	AcGCCTCAGA
msa134270.2{391_M732}	-----aaaaaaag	tcacgcgATTT	AAAAAAACTA	CAAAAAGCAT	AcGCCTCAGA
msa134270.2{391_M781}	-----aaaaaaag	tcacgcgATTT	AAAAAAACTA	CAAAAAGCAT	AcGCCTCAGA
msa134270.2{391_090}	-----	-----ATTT	AAAAAAACTA	CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_CJB110}	-----aaaaaaag	tcacgcgATTT	AAAAAAACTA	CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_1169NT}	-----aaaaaaag	tcacgcgATTT	AAAAAAACTA	CAAAAAGCAT	AcGCCTCAGA
msa134270.2{391_18RS21}	-----	-----gATTT	AAAAAAACTA	CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_2603}	atgaaaaaaag	tcacgcgATTT	AAAAAAACTA	CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_A909}	-----aaaaaaag	tcacgcgATTT	AAAAAAACTA	CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_JM9130013}	-----aaaaaaag	tcacgcgATTT	AAAAAAACTA	CAAAAAGCAT	AtGCCTCAGA
msa134270.2{391_H36B}	-----aaaaaaag	tcattgATTT	AAAAAAACTA	CAAAAAGCAT	AtGCCTCAGA
Consensus	***-----	-----****	*****	*****	*-*****

	51				100
msa134270.2{391_COH1}	AACtGTTTTA	AATAATATTA	ATTtGGAGGT	GTTTAAAGGa	GAAATAATTG
msa134270.2{391_M732}	AACtGTTTTA	AATAATATTA	ATTtGGAGGT	GTTTAAAGGa	GAAATAATTG
msa134270.2{391_M781}	AACtGTTTTA	AATAATATTA	ATTtGGAGGT	GTTTAAAGGa	GAAATAATTG
msa134270.2{391_090}	AACtGTTTTA	AATAATATTA	ATTtGGAGGT	GTTTAAAGGc	GAAATAATTG
msa134270.2{391_CJB110}	AACtGTTTTA	AATAATATTA	ATTtGGAGGT	GTTTAAAGGc	GAAATAATTG
msa134270.2{391_1169NT}	AACtGTTTTA	AATAATATTA	ATTtGGAGGT	GTTTAAAGGc	GAAATAATTG
msa134270.2{391_18RS21}	AACcGTTTTA	AATAATATTA	ATTtGGAGGT	GTTTAAAGGc	GAAATAATTG
msa134270.2{391_2603}	AACcGTTTTA	AATAATATTA	ATTtGGAGGT	GTTTAAAGGc	GAAATAATTG
msa134270.2{391_A909}	AACcGTTTTA	AATAATATTA	ATTtGGAGGT	GTTTAAAGGc	GAAATAATTG
msa134270.2{391_JM9130013}	AACcGTTTTA	AATAATATTA	ATTtGGAGGT	GTTTAAAGGc	GAAATAATTG
msa134270.2{391_H36B}	AACcGTTTTA	AATAATATTA	ATTtGGAGGT	GTTTAAAGGc	GAAATAATTG
Consensus	***-*****	*****	*****	*****	*****

	101				150
msa134270.2{391_COH1}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_M732}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_M781}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_090}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_CJB110}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_1169NT}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_18RS21}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_2603}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_A909}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_JM9130013}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
msa134270.2{391_H36B}	GATTAATAGG	ACCCTCTGGA	GCAGGGAAAT	CTACCTTGAT	TAAAACTATG
Consensus	*****	*****	*****	*****	*****

	151				200
msa134270.2{391_COH1}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_M732}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_M781}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_090}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_CJB110}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_1169NT}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_18RS21}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_2603}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_A909}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA

Table 76: Comparative Sequences relating to SAG0260

msa134270.2{391_JM9130013}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_H36B}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
Consensus	*****	*****	*****	*****	*****
	201				250
msa134270.2{391_COH1}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_M732}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_M781}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_090}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_CJB110}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_1169NT}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_18RS21}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_2603}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_A909}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_JM9130013}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_H36B}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
Consensus	*****	*-*****	*****	*****	*****
	251				300
msa134270.2{391_COH1}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_M732}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_M781}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_090}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_CJB110}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_1169NT}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_18RS21}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_2603}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_A909}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_JM9130013}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_H36B}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
Consensus	*****-*	***-*****	****-*****	*****	*****
	301				350
msa134270.2{391_COH1}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_M732}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_M781}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_090}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_CJB110}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_1169NT}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_18RS21}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_2603}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_A909}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_JM9130013}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
msa134270.2{391_H36B}	AAAATGAAAG	GTATTCAAAA	AACCTGAATTA	AAACAGCAGA	TAACCTCATAT
Consensus	*****	*****	*****	*****	*****
	351				400
msa134270.2{391_COH1}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_M732}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_M781}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_090}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_CJB110}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_1169NT}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_18RS21}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_2603}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_A909}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_JM9130013}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_H36B}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
Consensus	*****	*****	*****	*****	*****
	401				450
msa134270.2{391_COH1}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_M732}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_M781}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_090}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_CJB110}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_1169NT}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_18RS21}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_2603}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_A909}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_JM9130013}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_H36B}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
Consensus	*****	*****	*****	*****	*****
	451				500
msa134270.2{391_COH1}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_M732}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_M781}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_090}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_CJB110}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_1169NT}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_18RS21}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_2603}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC

Table 76: Comparative Sequences relating to SAG0260

msa134270.2{391_A909}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_JM9130013}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_H36B}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
Consensus	*****	*****	*****	*****	*****
msa134270.2{391_COH1}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_M732}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_M781}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_090}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_CJB110}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_1169NT}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_18RS21}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_2603}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_A909}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_JM9130013}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_H36B}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
Consensus	*****	*****	*****	*****	*****
msa134270.2{391_COH1}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_M732}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_M781}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_090}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_CJB110}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_1169NT}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_18RS21}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_2603}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_A909}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_JM9130013}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_H36B}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
Consensus	*****	*****	*****	*****	*****
msa134270.2{391_COH1}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_M732}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_M781}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_090}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_CJB110}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_1169NT}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_18RS21}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_2603}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_A909}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_JM9130013}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_H36B}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
Consensus	*****	*****	*****	*****	*****
msa134270.2{391_COH1}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	G-----
msa134270.2{391_M732}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_M781}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_090}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_CJB110}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_1169NT}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_18RS21}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_2603}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_A909}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_JM9130013}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
msa134270.2{391_H36B}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTCTTAA
Consensus	*****	*****	*****	*****	*****
msa134270.2{391_COH1}	AAGCTGAAGG	AGAA			
msa134270.2{391_M732}	AAGCTGAAGG	AGAA			
msa134270.2{391_M781}	AAGCTGAAGG	AGAA			
msa134270.2{391_090}	AAGCTGAAGG	AGAA			
msa134270.2{391_CJB110}	AAGCTGAAGG	AGAA			
msa134270.2{391_1169NT}	AAGCTGAAGG	AGAA			
msa134270.2{391_18RS21}	AAGCTGAAGG	AGAA			
msa134270.2{391_2603}	AAGCTGAAGG	AGAA			
msa134270.2{391_A909}	AAGCTGAAGG	AGAA			
msa134270.2{391_JM9130013}	AAGCTGAAGG	AGAA			
msa134270.2{391_H36B}	AAGCTGAAGG	AGAA			
Consensus	*****	****			

SEQ ID NO. 7612

STRAIN 2603 frame: 1

KKVIDLKKLQKAYASETVLNNINLEVPKGEIIGLIGPSGAGKSTLIKMLGMEKADKGTALVLDTPMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQIITHISKVVDLENQLDKFVSGSYSGMKRRSLALALLGNPTVLILDEPTVGIDPSLRRKIWQELINKDEGHSIFITTHVMDAEITSKVALLLRGNI AFDTPLHLKQFNV

SEQ ID NO. 7613

Table 76: Comparative Sequences relating to SAG0260

STRAIN 090 frame: 3
 LKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGTALVLD
 QMPDRNINLQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELKQIITHISKVVDLENQ
 LDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRKIWQELINIKDEGRSI
 FITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7614

STRAIN A909 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7615

STRAIN H36B frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7616

STRAIN 18RS21 frame: 1
 DLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGTALVLD
 TQMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQIITHISKVVDLEN
 QLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRKIWQELINIKDEGHS
 IFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7617

STRAIN M732 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALHESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7618

STRAIN COH1 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALHESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7619

STRAIN M781 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALHESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7620

STRAIN CJB110 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7621

STRAIN 1169NT frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7622

STRAIN JM9130013 frame: 1
 KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMGMKADKGT
 LVLDTQMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQIITHISKV
 DLENQLDKFVSGYSGGMRRLSLAIALLGNTVLILDEPTVGIDPSLRRKIWQELINIKD
 EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

PRETTY of: /biotmp/msa134470.2{*} April 10, 2003 02:16 ..

	1	50
msa134470.2{391_090}	-----LKKLQ KAYASETVLN NINLEVFKEI IIGLIGPSGA GKSTLIKTM	
msa134470.2{391_1169NT}	KKVIDLKKLQ KAYASETVLN NINLEVFKEI IIGLIGPSGA GKSTLIKTM	
msa134470.2{391_CJB110}	KKVIDLKKLQ KAYASETVLN NINLEVFKEI IIGLIGPSGA GKSTLIKTM	
msa134470.2{391_COH1}	KKVIDLKKLQ KAYASETVLN NINLEVFKEI IIGLIGPSGA GKSTLIKTM	
msa134470.2{391_M732}	KKVIDLKKLQ KAYASETVLN NINLEVFKEI IIGLIGPSGA GKSTLIKTM	
msa134470.2{391_M781}	KKVIDLKKLQ KAYASETVLN NINLEVFKEI IIGLIGPSGA GKSTLIKTM	
msa134470.2{391_18RS21}	----DLKKLQ KAYASETVLN NINLEVFKEI IIGLIGPSGA GKSTLIKTM	
msa134470.2{391_2603}	KKVIDLKKLQ KAYASETVLN NINLEVFKEI IIGLIGPSGA GKSTLIKTM	
msa134470.2{391_H36B}	KKVIDLKKLQ KAYASETVLN NINLEVFKEI IIGLIGPSGA GKSTLIKTM	
msa134470.2{391_JM9130013}	KKVIDLKKLQ KAYASETVLN NINLEVFKEI IIGLIGPSGA GKSTLIKTM	

Table 76: Comparative Sequences relating to SAG0260

msa134470.2{391_A909}	KKVIDLKKLQ	KAYASETVLN	NINLEVFKE	IIGLIGPSGA	GKSTLIKTML
Consensus	*****	*****	*****	*****	*****
	51				100
msa134470.2{391_090}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	aLENLLFFGK
msa134470.2{391_1169NT}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	aLENLLFFGK
msa134470.2{391_CJB110}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	aLENLLFFGK
msa134470.2{391_COH1}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALhESLT	gLENLLFFGK
msa134470.2{391_M732}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALhESLT	gLENLLFFGK
msa134470.2{391_M781}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALhESLT	gLENLLFFGK
msa134470.2{391_18RS21}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
msa134470.2{391_2603}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
msa134470.2{391_H36B}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
msa134470.2{391_JM9130013}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
msa134470.2{391_A909}	GMEKADKGTA	LVLDTQMPDh	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
Consensus	*****	*****	*****	*****	*****
	101				150
msa134470.2{391_090}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_1169NT}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_CJB110}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_COH1}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_M732}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_M781}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_18RS21}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_2603}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_H36B}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_JM9130013}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_A909}	MKGIOKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
Consensus	*****	*****	*****	*****	*****
	151				200
msa134470.2{391_090}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_1169NT}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_CJB110}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_COH1}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_M732}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_M781}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_18RS21}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGhSIFITTH	VMDEAELTSK
msa134470.2{391_2603}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGhSIFITTH	VMDEAELTSK
msa134470.2{391_H36B}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_JM9130013}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_A909}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
Consensus	*****	*****	*****	*****	*****
	201		224		
msa134470.2{391_090}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_1169NT}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_CJB110}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_COH1}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_M732}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_M781}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_18RS21}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_2603}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_H36B}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_JM9130013}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_A909}	VALLLRGNII	AFDTPLHLKK	QFNV		
Consensus	*****	*****	****		

Table 77: Comparative Sequences relating to SAG2059

SEQ ID NO. 7701

STRAIN 2603

TTGCCTATGTTGCTCTGTTGGTTTAGTTTTAGAGGGTGGCGGAATGAGAGGTCTTTATACT
GCTGGAGTTTTAGATGCTTTTCTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGTC
TCTGCTGCTGCTGCTGTTGTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGA
TACAATAAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGGTTTCGAACA
GGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCTATGAAATGGATGTATTT
GACGATGAAGCATTTAAAAAATCAAGTATTTGATTTTACGTAGTTGCTACAGAGATGACA
TCTGGTAAACCTGAATATTTTAAATTTGATAGTGTTTTGAACAAATGGAATTTTACGT
GCTAGTTTACGATTACAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
GATGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGATTTGACAAG
TTGATTTGTTGATGACTAGGCCGCTCAATTATCAGAAAAAGCCTTCAAGTGGACGATTG
TATAAACTCTGTATAGGAAATATCCTAATTTTGTAAAGACAGCCTCGAATCGGTACCAA
CAGTATAATAATAGTCTTGAAAAGGTCTGAGCCTTGAAAAACAGGCGATCTATTTGCA
ATTAGACCGAGTAAGAGCTTGGTTATTTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
AGTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTGAATAGTTAT
CTAATGAAA

SEQ ID NO. 7702

STRAIN 090

CCTATGTTGCTCTGTTGGTTTAGTTTTAG
AGGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTT
CTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGCTCTGCTGGTGC
ATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
ACAATAAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGG
TTTCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTC
TATGAAATTTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTG
ATTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTT
AAAATTGATAGTGTTTTGAACAAATGGAATTTTACGTGCTAGTTTCAGC
ATTACAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAG
ATGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGA
TTTGACAAGTTGATTTGTGTGATGACTAGGCCGCTCAATTATCAGAAAAA
GCCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATT
TTGTAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAA
AAGGTCTAGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCGAG
TAAGAGCTTGGTTATTTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATA
GTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTG
AATAGTTATCTAATGAAA

SEQ ID NO. 7703

STRAIN A909

CCTATGTTGCTCTGTTGGTTTAGTTTTAGAG
GGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTTCT
AGATGCAGGAATAAAAGTAGATGGTATCATATCTGCTCTGCTGGTGCAT
TGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATAC
AATAAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGGCT
TCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCTA
TGAAATTTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGAT
TTTTACGAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTTAA
AATTGATAGTGTTTTGAACAAATGGAATTTTACGTGCTAGTTTCAGCAT
TACCAGTAGTCTCAAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAGAT
GGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGAT
TGACAAGTTGATTTGTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGC
CTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTT
GTAAAGACAGCCTCGAACCCTGACCAACAGTATAATAATAGCCTTGAAAA
GGTCTAGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCAAGTA
AGAGCTTGGTTATTTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGT
ATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCTGAGCTGAA
TAGTTATCTAATGAAA

SEQ ID NO. 7704

STRAIN H36B

CCTATGTTGCTCTGTTGGTTTAGTTTTAG
AGGGTGGCGGAATGAGAGGTCTTTATACTGCTGGAGTTTTAGATGCTTTT
CTAGATGCAGGAATAAAAGTAGATGGTATCATATCTGCTCTGCTGGTGC
ATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
ACAATAAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGG
CTTCGAACAGGGAATTTTGTAAATAAAGATTTACCTATTATGAAGTTCCTA
TATGAAATTTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTG
ATTTTACGAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTT
AAAATTGATAGTGTTTTGAACAAATGGAATTTTACGTGCTAGTTTCAGC
ATTACAGTAGTCTCAAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAG
ATGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGA
TTTGACAAGTTGATTTGTGTGATGACTAGGCCGCTCAATTATCAGAAAAA
GCCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATT
TTGTAAGACAGCCTCGAACCCTGACCAACAGTATAATAATAGCCTTGAA
AAGGTCTAGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCAAG
TAAGAGCTTGGTTATTTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATA
GTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCTGAGCTG
AATAGTTATCTAATGAAA

SEQ ID NO. 7705

Table 77: Comparative Sequences relating to SAG2059

STRAIN 18RS21

CCTATGTTGTCGTGGTTTAGTTTAGAGG
 GTGGCGGAATGAGAGGTCCTTATACTGCTGGAGTTTATAGATGCTTTTCTA
 GATGCAGGAATAAAAAATAGATGGTATCGTATCTGTCTCTGCTGGTGCATT
 GTTTGGGTGTTAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATACA
 ATAAAAAGTATTTATCCCAACCCTAAATATATGAGTCTAAGGTCATGGTTT
 CGAACAGGGAATTTTGTAAATAAGATTTACCTATTATGAAGTTCCTAT
 GAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGATT
 TTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTAAA
 ATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTACGACATT
 ACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGATG
 GTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGATTT
 GACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGCC
 TTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTTG
 TAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAAAAG
 GTCATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCGAGTAA
 GAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGTA
 TTTATCAGCTTGGTATGAAAAGATGCTAAAAGTGTGATGCCTGAGCTGAAT
 AGTTATCTAATGAAA

SEQ ID NO. 7706

STRAIN M732

CCTATGTTGTCGTGGTTTAGTTTAGA
 GGGTGGCGGAATGAGAGGTCCTTATACTGCTGGAGTTTATAGATGCTTTTC
 TAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGCA
 TTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATA
 CAATAAAAAGTATTTATCCCAACCCTGAATATAAGTCTAAGATCATGGC
 TTCGAACAGGGAATTTTGTAAATAAGATTTACCTATTATGAAGTTCCT
 ATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGA
 TTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTA
 AAATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTACGCA
 TTACAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGA
 TGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGAT
 TTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAG
 CCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTT
 TGTAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAAA
 AGGTATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCGAGT
 AAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAG
 TATTATCAGCTTGGTATGAAAATATGCTAAAAGTGTGATGCCTGAGCTGA
 ATAGTTATCTAATGAAA

SEQ ID NO. 7707

STRAIN COH1

CCTATGTTGTCGTGGTTTAGTTTAA
 GAGGTGGCGGAATGAGAGGTCCTTATACTGCTGGAGTTTATAGATGCTTT
 TCTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTG
 CATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGA
 TACATAAAAAGTATTTATCCCAACCCTGAATATATGAGTCTAAGATCATG
 GCTTCGAACAGGGAATTTTGTAAATAAGATTTACCTATTATGAAGTTC
 CTATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATT
 GATTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTT
 TAAATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTACG
 CATTACAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
 GATGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGG
 ATTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAA
 AGCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAAT
 TTTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGA
 AAAGTATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCGA
 GTAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
 AGTATTTATCAGCTTGGTATGAAAATATGCTAAAAGTGTGATGCCTGAGCT
 GAATAGTTATCTAATGAAA

SEQ ID NO. 7708

STRAIN M781

CCTATGTTGTCGTGGTTTAGTTTAG
 AGGGTGGCGGAATGAGAGGTCCTTATACTGCTGGAGTTTATAGATGCTTTT
 CTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGC
 ATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
 ACAATAAAAAGTATTTATCCCAACCCTGAATATAAGTCTAAGATCATGG
 CTTTGAACAGGGAATTTTGTAAATAAGATTTACCTATTATGAAGTTC
 TATGAAATTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTG
 ATTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTT
 AAAATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTACG
 ATTACAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAG
 ATGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGA
 TTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAA
 GCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAAT
 TTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGA
 AAAGTATGAGCCTTGAAAAACAGGCGATCTATTTGCAATTAGACCGA
 GTAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
 GTATTTATCAGCTTGGTATGAAAATATGCTAAAAGTGTGATGCCTGAGCTG
 AATAGTTATCTAATGAAA

Table 77: Comparative Sequences relating toSAG2059

SEQ ID NO. 7709

STRAIN CJB110

CCTATGTTGTCGTGGTTTGTAGTTTAA
 GAGGGTGGCGGAATGAGAGGCTTTTATACTGCTGGAGTTTGTAGATGCTTT
 TCTAGATGCAGGAATAAAATAGATGGTATCGTATCTGTCTCTGCTGGTG
 CATTTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGA
 TACAATAAAAAGTATTTATCCACCCCTAAATATATGAGTCTAAGGTCATG
 GTTTCGAAACAGGAATTTTGTAAATAAGATTTCACCTATTATGAAGTTC
 CTATGAAATTGGATGTATTTGACGATGAAGCATTAAAAAATCAAGTATT
 GATTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTT
 TAAATTTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTCAG
 CATACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
 GATGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTAGG
 ATTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAA
 AGCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAAT
 TTTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGA
 AAAGGTCATGAGCCTTGAAAAAACAGGCGATCTATTGCAATTAGACCGA
 GTAAGAGCTTGGTTATTTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
 AGTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCT
 GAATAGTTATCTAATGAAA

SEQ ID NO. 7710

STRAIN 1169NT

CCTATGTTGTCGTGGTTTGTAGTTTGTAGGGTG
 GCGGAATGAGAGGCTTTTATACTGCTGGAGTTTGTAGATGCTTTTCTAGAT
 GCAGGAATAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGCATTGTT
 TGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATACAATA
 AAAAGTATTTATCCACCCCTAAATATATGAGTCTAAGATCATGGCTTCGA
 ACAGGGAATTTTGTAAATAAGATTTCACCTATTATGAAGTTCCCTATGAA
 ATTGGATGTATTTGACGATGAAGCATTAAAAAATCAAGTATTGATTTT
 ACGCAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTAAATTT
 GATAGTGTCTTTGAACAAATGGAAATTTTACGTGCTAGTTTCAGCAATTACC
 AGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGATGGTG
 GTTTATCTGATAGTATCCCGTTGATTTTGCCCGTGGTTTAGGATTTGAC
 AAGTTGATTTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGCCTTC
 AAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTTGTAA
 AGACAGCCTCGAATCGGTACCAACAGTATAATAATAGCCTTGAAAAGGTC
 ATGAGCCTTGAAAAAACAGGCGATCTATTGCAATTAGGCCGAGTAAAAAG
 CTTGGTTATTGTCGCTTAGAGAAGAATCCGGATAAACTTGATAGTATTT
 ATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTGAATAGT
 TATCTAATGAAA

SEQ ID NO. 7711

STRAIN JM9130013

CCTATGTTGTCGTGGTTTGTAGTTTGTAGAG
 GGTGGCGGAATGAGAGGCTTTTATACTGCTGGAGTTTGTAGATGCTTTTCT
 AGATGCAGGAATAAAGTAGATGGTATCATATCTGTCTCTGCTGGTGCA
 TGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATAC
 AATAAAAAGTATTTATCCACCCCTAAATATATGAGTCTAAGGTCATGGCT
 TCGAACAGGGAATTTTGTAAATAAGATTTCACCTATTATGAAGTTCCCTA
 TGAAATTGGATGTATTTGACGATGAAGCATTAAAAAATCAAGTATTGAT
 TTTTACGCGATTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTTAA
 AATTGATAGTGTTTTGAACAAATGGAAATTTTACGTGCTAGTTTCAGCAT
 TACCAGTAGTCTCAAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAGAT
 GGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCCGTGGTTTAGGATT
 TGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGC
 CTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTT
 GTAAAGACAGCCTCGAACCCTGACCAACAGTATAATAATAGCCTTGAAAA
 GGTATGAGCCTTGAAAAAACAGGCGATCTATTGCAATTAGACCAAGTA
 AGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGT
 ATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCTGAGCTGAA
 TAGTTATCTAATGAAA

PRETTY of: /biotmp/msa47199.2{*} February 19, 2003 05:51 ..

	1		50
msa47199.2{394_A909}	----CCTATGT	TGTCGTGGTGG	TTTAGTTTAA
msa47199.2{394_H36B}	----CCTATGT	TGTCGTGGTGG	TTTAGTTTAA
msa47199.2{394_JM9130013}	----CCTATGT	TGTCGTGGTGG	TTTAGTTTAA
msa47199.2{394_090}	----CCTATGT	TGTCGTGGTGG	TTTAGTTTAA
msa47199.2{394_18RS21}	----CCTATGT	TGTCGTGGTGG	TTTAGTTTAA
msa47199.2{394_2603}	ttgCCTATGT	TGTCGTGGTGG	TTTAGTTTAA
msa47199.2{394_CJB110}	----CCTATGT	TGTCGTGGTGG	TTTAGTTTAA
msa47199.2{394_COH1}	----CCTATGT	TGTCGTGGTGG	TTTAGTTTAA
msa47199.2{394_M732}	----CCTATGT	TGTCGTGGTGG	TTTAGTTTAA
msa47199.2{394_M781}	----CCTATGT	TGTCGTGGTGG	TTTAGTTTAA
msa47199.2{394_1169NT}	----CCTATGT	TGTCGTGGTGG	TTTAGTTTAA
Consensus	*****	*****	*****
	51		100
msa47199.2{394_A909}	TCCTTATACT	GCTGGAGTTT	TAGATGCTTT
msa47199.2{394_H36B}	TCCTTATACT	GCTGGAGTTT	TAGATGCTTT
msa47199.2{394_JM9130013}	TCCTTATACT	GCTGGAGTTT	TAGATGCTTT

Table 77: Comparative Sequences relating toSAG2059

msa47199.2{394_090}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_18RS21}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_2603}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_CJB110}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_COH1}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_M732}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_M781}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_1169NT}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	TAGATGGTAT	CaTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_H36B}	TAGATGGTAT	CaTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_JM9130013}	TAGATGGTAT	CaTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_090}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_18RS21}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_2603}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_CJB110}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_COH1}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_M732}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_M781}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_1169NT}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAAATTTT
Consensus	*****	*-*****	*****-****	*****	*****
msa47199.2{394_A909}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_H36B}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_JM9130013}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_090}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_18RS21}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_2603}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_CJB110}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_COH1}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_M732}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_M781}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_1169NT}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATTTTATC
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_H36B}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_JM9130013}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_090}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_18RS21}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_2603}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_CJB110}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_COH1}	CCACCCTgAA	TATATGAGTC	TAAGaTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_M732}	CCACCCTgAA	TATATGAGTC	TAAGaTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_M781}	CCACCCTgAA	TATATGAGTC	TAAGaTCATG	GcTTcGAACA	GGGAATTTTG
msa47199.2{394_1169NT}	CCACCCTaAA	TATATGAGTC	TAAGaTCATG	GcTTcGAACA	GGGAATTTTG
Consensus	*****-**	*****	*****-*****	*-*****	*****
msa47199.2{394_A909}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_H36B}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_JM9130013}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_090}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_18RS21}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_2603}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_CJB110}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_COH1}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_M732}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_M781}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_1169NT}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_H36B}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_JM9130013}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_090}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_18RS21}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_2603}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_CJB110}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_COH1}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_M732}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_M781}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_1169NT}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
Consensus	*****	*****	*****	*****	-*****
msa47199.2{394_A909}	AGAGATGACA	TCGGGTAAAC	CTGAgTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_H36B}	AGAGATGACA	TCGGGTAAAC	CTGAgTATTT	TAAAATTGAT	AGTGTtTTTG

Table 77: Comparative Sequences relating toSAG2059

msa47199.2{394_JM9130013}	AGAGATGACA	TCTGGTAAAC	CTGAgTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_090}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_18RS21}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_2603}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_CJB110}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_COH1}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_M732}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_M781}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_1169NT}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
Consensus	*****	*****	*****	*****	*****
401					
msa47199.2{394_A909}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_H36B}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_JM9130013}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_090}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_18RS21}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_2603}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_CJB110}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_COH1}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_M732}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_M781}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_1169NT}	AACAAATGGA	AATTTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
Consensus	*****	*****	*****	*****	*****
451					
msa47199.2{394_A909}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_H36B}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_JM9130013}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_090}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_18RS21}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_2603}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_CJB110}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_COH1}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_M732}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_M781}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_1169NT}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
Consensus	*****	*****	*****	*****	*****
501					
msa47199.2{394_A909}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_H36B}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_JM9130013}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_090}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_18RS21}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_2603}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_CJB110}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_COH1}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_M732}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_M781}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
msa47199.2{394_1169NT}	TATtCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTGACAAG	TTGATTGTTG
Consensus	***-*****	*****	*****	*****	*****
551					
msa47199.2{394_A909}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_H36B}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_JM9130013}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_090}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_18RS21}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_2603}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_CJB110}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_COH1}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_M732}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_M781}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_1169NT}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
Consensus	*****	*****	*****	*****	*****
601					
msa47199.2{394_A909}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_H36B}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_JM9130013}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_090}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_18RS21}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_2603}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_CJB110}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_COH1}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_M732}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_M781}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_1169NT}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
Consensus	*****	*****	*****	*****	*****
651					
msa47199.2{394_A909}	cCGGTACCAA	CAGTATAATA	ATAGcCTTGA	AAAGGTCATG	AGCCTTGAAA

Table 77: Comparative Sequences relating to SAG2059

msa47199.2{394_H36B}	cCGGTACCAA	CAGTATAATA	ATAGcCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_JM9130013}	cCGGTACCAA	CAGTATAATA	ATAGcCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_090}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_18RS21}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_2603}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_CJB110}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_COH1}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_M732}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_M781}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_1169NT}	tCGGTACCAA	CAGTATAATA	ATAGcCTTGA	AAAGGTCATG	AGCCTTGAAA
Consensus	*****	*****	****-****	*****	*****
msa47199.2{394_A909}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCaA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_H36B}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCaA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_JM9130013}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCaA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_090}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_18RS21}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_2603}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_CJB110}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_COH1}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_M732}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_M781}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_1169NT}	AAACAGGCGA	TCTATTTGCA	ATTAGgCCgA	GTAAaAGCTT	GGTTATTGtC
Consensus	*****	*****	*****-*-*	*****	*****-*
msa47199.2{394_A909}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_H36B}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_JM9130013}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_090}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_18RS21}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_2603}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_CJB110}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_COH1}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_M732}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_M781}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_1169NT}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	GAAAGATGCT	AAAAGTGgGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_H36B}	GAAAGATGCT	AAAAGTGgGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_JM9130013}	GAAAGATGCT	AAAAGTGgGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_090}	GAAAGATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_18RS21}	GAAAGATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_2603}	GAAAGATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_CJB110}	GAAAGATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_COH1}	GAAAtATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_M732}	GAAAtATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_M781}	GAAAtATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_1169NT}	GAAAGATGCT	AAAAGTGtGA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
Consensus	****-*****	*****-*	*****	*****	*****

SEQ ID NO. 7712

STRAIN 2603 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERLRY
 NKKYLSHPKYMSLRSWRTGNFVNKDFTYEYVPMKLDVDFDEAFKSSIDFYVVAATEMTS
 GKPEYFKIDSVEQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IIVMTRLPNYQKKPSSGRLYKTLRYKYPNFVKTASNRYQQYNNLSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPKLDSIYQLGMKDAKSMPELNSYLMK

SEQ ID NO. 7713

STRAIN 090 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERLRY
 NKKYLSHPKYMSLRSWRTGNFVNKDFTYEYVPMKLDVDFDEAFKSSIDFYVVAATEMTS
 GKPEYFKIDSVEQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IIVMTRLPNYQKKPSSGRLYKTLRYKYPNFVKTASNRYQQYNNLSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPKLDSIYQLGMKDAKSMPELNSYLMK

SEQ ID NO. 7714

STRAIN A909 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKVDGIIISVSAGALFGVNFVSRQRERLRY
 NKKYLSHPKYMSLRSWRTGNFVNKDFTYEYVPMKLDVDFDEAFKSSIDFYAVATEMTS
 GKPEYFKIDSVEQMEILRASSALPVVSKMVDWQKKYLDGGLSDSIPVDFARGLGFDKL
 IIVMTRLPNYQKKPSSGRLYKTLRYKYPNFVKTASNRYQQYNNLSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPKLDSIYQLGMKDAKSMPELNSYLMK

SEQ ID NO. 7715

STRAIN H36B frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKVDGIIISVSAGALFGVNFVSRQRERLRY
 NKKYLSHPKYMSLRSWRTGNFVNKDFTYEYVPMKLDVDFDEAFKSSIDFYAVATEMTS

Table 77: Comparative Sequences relating toSAG2059

GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQGGKYLDDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7716

STRAIN 18RS21 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKKYLSHPKYMSLRSWLRTGNFVNKDFTYYEVPKMLDVFDDFAFKKSSIDFYVVAATEMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQGGKYLDDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7717

STRAIN M732 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKKYLSHPKYMSLRSWLRTGNFVNKDFTYYEVPKMLDVFDDFAFKKSSIDFYVVAATEMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQGGKYLDDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7718

STRAIN COH1 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKKYLSHPKYMSLRSWLRTGNFVNKDFTYYEVPKMLDVFDDFAFKKSSIDFYVVAATEMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQGGKYLDDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7719

STRAIN M781 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKKYLSHPKYMSLRSWLRTGNFVNKDFTYYEVPKMLDVFDDFAFKKSSIDFYVVAATEMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQGGKYLDDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7720

STRAIN CJB110 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKKYLSHPKYMSLRSWLRTGNFVNKDFTYYEVPKMLDVFDDFAFKKSSIDFYVVAATEMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQGGKYLDDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7721

STRAIN JM9130013 frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKVDGIISVSAGALFGVNFVSRQRERALRY
 NKKYLSHPKYMSLRSWLRTGNFVNKDFTYYEVPKMLDVFDDFAFKKSSIDFYVVAATEMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQGGKYLDDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7722

STRAIN 1169NT frame: 1

PMLSVGLVLEGGMRGLYTAGVLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKKYLSHPKYMSLRSWLRTGNFVNKDFTYYEVPKMLDVFDDFAFKKSSIDFYVVAATEMTS
 GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQGGKYLDDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKASNRYQQYNNSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPDKLDISIYQLGMKDAKSGMPELNSYLMK

	1				50
msa47322.2{394_A909}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG	IKVDGIISVS	AGALFGVNFV
msa47322.2{394_H36B}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG	IKVDGIISVS	AGALFGVNFV
msa47322.2{394_JM9130013}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG	IKVDGIISVS	AGALFGVNFV
msa47322.2{394_090}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG	IKIDGIVSVS	AGALFGVNFV
msa47322.2{394_1169NT}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG	IKIDGIVSVS	AGALFGVNFV
msa47322.2{394_18RS21}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG	IKIDGIVSVS	AGALFGVNFV
msa47322.2{394_2603}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG	IKIDGIVSVS	AGALFGVNFV
msa47322.2{394_CJB110}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG	IKIDGIVSVS	AGALFGVNFV
msa47322.2{394_COH1}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG	IKIDGIVSVS	AGALFGVNFV
msa47322.2{394_M732}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG	IKIDGIVSVS	AGALFGVNFV
msa47322.2{394_M781}	PMLSVGLVLE	GGGMRGLYTA	GVLDAGFLDAG	IKIDGIVSVS	AGALFGVNFV
Consensus	*****	*****	*****	***-***-***	*****
	51				100
msa47322.2{394_A909}	SRQRERALRY	NKKYLSHPKY	MSLSRWLRTG	NFVNKDFTYY	EVPKMLDVFD
msa47322.2{394_H36B}	SRQRERALRY	NKKYLSHPKY	MSLSRWLRTG	NFVNKDFTYY	EVPKMLDVFD
msa47322.2{394_JM9130013}	SRQRERALRY	NKKYLSHPKY	MSLSRWLRTG	NFVNKDFTYY	EVPKMLDVFD
msa47322.2{394_090}	SRQRERALRY	NKKYLSHPKY	MSLSRWLRTG	NFVNKDFTYY	EVPKMLDVFD
msa47322.2{394_1169NT}	SRQRERALRY	NKKYLSHPKY	MSLSRWLRTG	NFVNKDFTYY	EVPKMLDVFD
msa47322.2{394_18RS21}	SRQRERALRY	NKKYLSHPKY	MSLSRWLRTG	NFVNKDFTYY	EVPKMLDVFD

Table 77: Comparative Sequences relating to SAG2059

msa47322.2{394_2603}	SRQRERALRY	NKKYLShpKy	MSLRswfRTG	NFVNkdFTYY	EVPMKLDVFD
msa47322.2{394_CJB110}	SRQRERALRY	NKKYLShpKy	MSLRswfRTG	NFVNkdFTYY	EVPMKLDVFD
msa47322.2{394_COH1}	SRQRERALRY	NKKYLShPeY	MSLRswlRTG	NFVNkdFTYY	EVPMKLDVFD
msa47322.2{394_M732}	SRQRERALRY	NKKYLShPeY	MSLRswlRTG	NFVNkdFTYY	EVPMKLDVFD
msa47322.2{394_M781}	SRQRERALRY	NKKYLShPeY	MSLRswlRTG	NFVNkdFTYY	EVPMKLDVFD
Consensus	*****	*****-*	*****-***	*****	*****
msa47322.2{394_A909}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_H36B}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_JM9130013}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_090}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_1169NT}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_18RS21}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_2603}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_CJB110}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_COH1}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_M732}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
msa47322.2{394_M781}	DEAFKKSSID	FYaVATEMTS	GKPEYFKIDS	VFEQMEILRA	SSALPVVSKM
Consensus	*****	**_*****	*****	*****	*****
msa47322.2{394_A909}	VvWQgKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_H36B}	VvWQgKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_JM9130013}	VvWQgKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_090}	VdWQgKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_1169NT}	VdWQgKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_18RS21}	VdWQgKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_2603}	VdWQgKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_CJB110}	VdWQgKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_COH1}	VdWQgKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_M732}	VdWQgKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
msa47322.2{394_M781}	VdWQgKKYLD	GGLSDSIPVD	FARGLGFDKL	IVVMTRPLNY	QKKPSSGRLY
Consensus	*_******	*****	*****	*****	*****
msa47322.2{394_A909}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIGR
msa47322.2{394_H36B}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIGR
msa47322.2{394_JM9130013}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIGR
msa47322.2{394_090}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIGR
msa47322.2{394_1169NT}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIGR
msa47322.2{394_18RS21}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIGR
msa47322.2{394_2603}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIGR
msa47322.2{394_CJB110}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIGR
msa47322.2{394_COH1}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIGR
msa47322.2{394_M732}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIGR
msa47322.2{394_M781}	KTLYRKYPNF	VKTASNRYQQ	YNNsLEKVMS	LEKTGDLFAI	RPSKSLVIGR
Consensus	*****	*****	*****	*****	*****_*
msa47322.2{394_A909}	LEKNPDKLDS	IYQLGMKdAK	SgMPELNSYL	MK	
msa47322.2{394_H36B}	LEKNPDKLDS	IYQLGMKdAK	SgMPELNSYL	MK	
msa47322.2{394_JM9130013}	LEKNPDKLDS	IYQLGMKdAK	SgMPELNSYL	MK	
msa47322.2{394_090}	LEKNPDKLDS	IYQLGMKdAK	SvMPELNSYL	MK	
msa47322.2{394_1169NT}	LEKNPDKLDS	IYQLGMKdAK	SvMPELNSYL	MK	
msa47322.2{394_18RS21}	LEKNPDKLDS	IYQLGMKdAK	SvMPELNSYL	MK	
msa47322.2{394_2603}	LEKNPDKLDS	IYQLGMKdAK	SvMPELNSYL	MK	
msa47322.2{394_CJB110}	LEKNPDKLDS	IYQLGMKdAK	SvMPELNSYL	MK	
msa47322.2{394_COH1}	LEKNPDKLDS	IYQLGMKyAK	SvMPELNSYL	MK	
msa47322.2{394_M732}	LEKNPDKLDS	IYQLGMKyAK	SvMPELNSYL	MK	
msa47322.2{394_M781}	LEKNPDKLDS	IYQLGMKyAK	SvMPELNSYL	MK	
Consensus	*****	*****_*	*_******	**	

Table 78: Comparative Sequences relating to SAG1016

SEQ ID NO. 7801

STRAIN 2603

ATGAAAGTTTGTAGTTGATGATGAACCAAGTTGCACGTAACGAATTAATTTACCTTCTT
 AATAAGATGATTTCTAACCTCGTTATAGCAGAGGCGCATGATATGGCTACTGCATTAGCT
 ATTTTACTTAGAGAACTTTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCT
 GGGTTGCAATTAGCAGAGTATATCAATAAAATGCCAAACCACCATTTATGATATTTGCG
 ACTGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCATGATGCGCGTGATTATTTGTTA
 AAACCCCTATGATTTTGATAGGCTAAAGCAAGCTATGGATAGAGTAAAGGAGCGCTAAGT
 ACATCTACAATATATAGAGAGCGTAACCTCCGGTCTCTCTTCAAGCAACAGTATCCATTG
 ACAGTAGAAGATCGAATCTATCTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATG
 CAAGGAAAACTGATTATACAAACACCTGATAAAAAATTATGAAATTGATGGCTCTCTACAA
 CAATGGCAAGATAAATACCATCATCTCAATTTGTACGGGTACATCGCTCTTACATTGTG
 AACATTAATGCTATTAAACGATTGAACCTTGGTTTAAACCAACACTTCAGTTACACCTT
 TGTATAAAATAACAGTTCCTGTTAGCAGAGCAATGTAAACCCCTAAACAAATGTTA
 GGCATATCTACC

SEQ ID NO. 7802

STRAIN 090

AAAGTTTGTAGTTGATGATGAACCAAGTTGCACGTAA
 CGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAG
 AGGCGCATGATATGGCTACTGCAATAGCTATTTTACTTAGAGAACTTTT
 GATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATT
 AGCAGAGTATATCAATAAAATGCCAAACCACCATTTATGATATTTGCGA
 CTGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCATGATGCGCGTGAT
 TATTTGTAAACCCCTATGATTTTGATAGGCTAAAGCAAGCTATGGATAG
 AGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTCCG
 GTCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTAT
 CTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACT
 GATTATACAAACACCTGATAAAAAATTATGAAATTGATGGCTCTCTACAAC
 AATGGCAAGATAAATACCATCATCTCAATTTGTACGGGTACATCGCTCT
 TACATTGTGAACATTAATGCTATTAAACGATTGAACCTTGGTTTAAACCA
 AACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAGAG
 CAAATGTAAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7803

STRAIN A909

AAAGTTTGTAGTTGATGATGAACCAAGTTGCACGTAA
 GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAGA
 GCGCGCATGATATGGCTACTGCAATAGCTATTTTACTTAGAGAACTTTT
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
 GCAGAGTATATCAATAAAATGCCAAACCACCATTTATGATATTTGCGGAC
 TGCTTATGATCAATATGCTATTCAAGCTTTTGAGCATGATGCGCGTGATT
 ATTTGTTAAACCCCTATGAGTTTGATAGGCTAAAGCAAGCTATGGATAGA
 GTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTCCGG
 CCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
 TGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACTG
 ATTATACAAACACCTGATAAAAAATTATGAAATTGATGGCTCTCTACAACA
 ATGGCAAGATAAATACCATCATCTCAATTTGTACGGGTGACCGCTCTT
 ACATTGTGAATATTAATGCTATTAAACGATTGAACCTTGGTTTAAACCA
 ACACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAGAGC
 AAATGTAAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7804

STRAIN H36B

AAAGTTTGTAGTTGATGATGAACCAAGTTGCACGT
 AACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGC
 AGAGGCGCATGATATGGCTACTGCAATAGCTATTTTACTTAGAGAACTTT
 TTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAA
 TTAGCAGAGTATATCAATAAAATGCCAAACCACCATTTATGATATTTGCG
 GACTGCTTATGATCAATATGCTATTCAAGCTTTTGAGCATGATGCGCGTG
 ATTATTTGTTAAACCCCTATGAGTTTGATAGGCTAAAGCAAGCTATGGAT
 AGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTTC
 CGGCCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCT
 ATCTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAA
 CTGATTATACAAACACCTGATAAAAAATTATGAAATTGATGGCTCTCTACA
 ACAATGGCAAGATAAATACCATCATCTCAATTTGTACGGGTGACCGCT
 CTTACATTGTGAATATTAATGCTATTAAACGATTGAACCTTGGTTTAAAC
 CAAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAG
 AGCAATGTAAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7805

STRAIN 18RS21

AAAGTTTGTAGTTGATGATGAACCAAGTTGCACGTAA
 GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAGA
 GCGCGCATGATATGGCTACTGCAATAGCTATTTTACTTAGAGAACTTTT
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
 GCAGAGTATATCAATAAAATGCCAAACCACCATTTATGATATTTGCGAC
 TGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCATGATGCGCGTGATT
 ATTTGTTAAACCCCTATGATTTTGATAGGCTAAAGCAAGCTATGGATAGA
 GTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACCTCCGG
 TCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
 TGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACTG

Table 78: Comparative Sequences relating to SAG1016

ATTATACAAACACCTGATAAAATTTATGAAATTTGATGGCTCTCTACAACA
 ATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCTT
 ACATTTGTGAACATTAAATGCTATTAAAAACGATTGAACCTTGGTTTAAACCAA
 ACATTTGAGTTACACCTTTGTAATAAAATAACAGTTCTCTGTTAGCAGAGC
 AAATGTAAACCCCTAAACCAAATGTTAGGCATATCTACC

SEQ ID NO. 7806

STRAIN M732

AAAGTTTTAGTAGTTGATGATGAACCAAGTT
 GCACGTAACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGT
 TATAGCAGAGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAG
 AAATTTTGTAGTAGCCTGTTAGATATCCATCTCAGAGATGATTCTGGG
 TTGCAATTAGCAGAGTATATCAATAAAATGCCAAACCAACATTATTGAT
 ATTCGCGACTGCTTATGATCAATATGCTATTCAAGGCTTTTGAGCAGGATG
 CGCGTATTAATTTGTTAAACCCCTATGAGTTTGTAGGTTAAAGCAAGCT
 ATGGATAGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGT
 AGCTTCCGGTCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATC
 GAATCTATCTGGTGTGCGCGGATGATATCCCTTTTGATTGAAGCTATGCAA
 GGAAAACTGATTATACAAACACCTGATAAAAAATTATGAAATTTGATGGCTC
 TCTACAACAAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTAC
 ATCGCTCTTACATTGTGAATATTAATGCTATTAAACGATTGAACCTTGG
 TTTAACCAACACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCTCTGT
 TAGCAGAGCAATGTAAACCCCTAAACCAAATGTTAGGCATATCTACC

SEQ ID NO. 7807

STRAIN COH1

AAAGTTTTAGTAGTTGATGATGAACCAAGTTGCACGTA
 ACCAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCA
 GAGGCGCATGATATGGCTACTGCTATTAGCTATTTTACTTAGAGAACTTT
 TGATGTAGCCTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAAT
 TAGCAGAGTATATCAATAAAATGCCAAACCAACATTATTGATATTCGCG
 ACTGCTTATGATCAATATGCTATTCAAGGCTTTTGAGCAGGATGCGCGTGA
 TTATTTGTTAAACCCCTATGAGTTTGTAGGTTAAAGCAAGCTATGGATA
 GAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAGCTTCC
 GGTCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTA
 TCTGGTGTGCGCGGATGATATCCCTTTTGATTGAAGCTATGCAAGGAAAC
 TGATTATACAAACACCTGATAAAAAATTATGAAATTTGATGGCTCTCTACAA
 CAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTC
 TTACATTGTGAATATTAATGCTATTAAACGATTGAACCTTGGTTTAAACC
 AAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCTCTGTTAGCAGA
 GCAATGTAAACCCCTAAACCAAATGTTAGGCATATCTACC

SEQ ID NO. 7808

STRAIN M781

AAAGTTTTAGTAGTTGATGATGAACCAAGTTGCACGTAAC
 GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAGA
 GGGCGCATGATATGGCTACTGCTATTAGCTATTTTACTTAGAGAACTTTTG
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
 GCAGAGTATATCAATAAAATGCCAAACCAACATTATTGATATTCGCGAC
 TGCTTATGATCAATATGCTATTCAAGGCTTTTGAGCAGGATGCGCGTGAAT
 ATTTGTTAAAAACCCCTATGAGTTTGTAGGTTAAAGCAAGCTATGGATAGA
 GTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAGCTTCCGG
 TCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
 TGGTGTGCGCGGATGATATCCCTTTTGATTGAAGCTATGCAAGGAAACCTG
 ATTATACAAACACCTGATAAAAAATTATGAAATTTGATGGCTCTCTACAACA
 ATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCTT
 ACATTGTGAATATTAATGCTATTAAACGATTGAACCTTGGTTTAAACCAA
 ACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCTCTGTTAGCAGAGC
 AAATGTAAACCCCTAAACCAAATGTTAGGCATATCTACC

SEQ ID NO. 7809

STRAIN CJB110

CTTAATAAGTATGATTCTAACCTCGTTATAGCAGAGGCGCATGATATGGC
 TACTGCATTAGCTATTTTACTTAGAGAACTTTTGATGTAGCACTGTTAG
 ATATCCATCTCAGAGATGATTCTGGGTTGCAATTAGCAGAGTATATCAAT
 AAAATGCCAAACCAACATTATTGATATTCGCGACTGCTTATGATCAATA
 TGCTATTCAAGCTTTTGAGCATGATGCGCGTGAATTTGTTAAAAACCTT
 ATGAGTTTGTAGGCTAAAGCAAGTATGGATAGAGTAAAGGAGCGCTA
 AGTACATCTACAATTATAGAGAGCGTAACCTTCCGGCCCTCTCTCAAGCA
 ACAGTATCCATTGACAGTAGAAGATGAAATCTATCTGGTGTGCGCGGATG
 ATATCTCTTTGATTGAAGCTATGCAAGGAAACCTGATTATACAAACACCT
 GATAAAAAATTATGAAATTTGATGGCTCTCTACAACAATGGCAAGATAAACT
 ACCATCATCTCAATTTGTACGGGTGCAACCGCTCTTACATTGTGAATATTA
 ATGCTATTAACGAGTTGAACCTTGGTTTAAACCAACACTTCAGTTACAC
 CTTTGTAAATAAAATAACAGTTCTCTGTTAGCAGAGCAATGTAAACCCCT
 AAAACAAATGTTAGG

SEQ ID NO. 7810

STRAIN 1169NT

AAAGTTTTAGTAGTTGATGATGAACCAAG
 TTGCACGTAACGAATTAATTTATCTTCTTAATAAGTATGATTCTAACCTC
 GTTATAGCAGAGGCGCATGATATAGCTACTGCATTAGCTATTTTACTTAG

Table 78: Comparative Sequences relating to SAG1016

AGAAACTTTTGTAGTACTGTTAGATATCCATCTCAGAGATGATTCTG
GGTTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCACTTATG
ATATTCCGCACTGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCATGA
TGCCTGTGATTATTTGTTAAACCCCTATGAGTTTGATAGGCTAAAGCAAG
CTATGGATAGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGC
GTAACCTCCGCCCCCTCTCTCAAGCAACAGTATCCATTGACAGTAGAAGA
TCGAATCTATCTGGTTCGGCGGATGATATCCTTTTGATTGAAGCTATGC
AAGGAAAACGTATTATACAAACACCTGATAAAAATTATGAAATTGATGGC
TCTCTACAACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGT
GCACCGCTCTTACATTGTGAATATTAATGCTATTAACAGATTGAACCTT
GGTTTAAACCAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCTC
GTTAGCAGAGCAAATGTAAACCCCTAAACAAATGTTAGGCATATCTAC
C

SEQ ID NO. 7811

STRAIN JM9130013

AAAGTTTGTAGTGTAGTGAACCACT

TGCACGTAAACGAATTAATTACCTTCTTAATAAGTATGATTCTAACCTCG
TTATAGCAGAGGCGCATGATATGGCTACTGCAATTAGCTATTTACTTAGA
GAAACTTTTGTAGTACTGTTAGATATCCATCTCAGAGATGATTCTGG
GTTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCACTTATGTA
TATTCCGCACTGCTTATGATCAATATGCTATTCAAGCTTTTGAGCATGAT
GCGCGTGTATTATTTGTTAAACCCCTATGAGTTTGATAGGCTAAAGCAAGC
TATGGATAGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCG
TAACCTCCGCCCCCTCTCTCAAGCAACAGTATCCATTGACAGTAGAAGAT
CGAATCTATCTGGGTGTCGGCGGATGATATCCTTTTGATTGAAGCTATGCA
AGGAAAACCTGATTATACAAACACCTGATAAAAATTATGAAATTGATGGCT
CTCTACACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTG
CACCGCTCTTACATTGTGAATATTAATGCTATTAACAGATTGAACCTTG
GTTTAAACCAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCTC
TTAGCAGAGCAAATGTAAACCCCTAAACAAATGTTAGGCATATCTACC

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa141507.2{*} April 10, 2003 06:36 ..

	1		50
msa141507.2{399_A909}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_CJB110}	-----	-----	-----
msa141507.2{399_H36B}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_JM9130013}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_1169NT}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_090}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_18RS21}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_2603}	atgaaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_COH1}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_M732}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
msa141507.2{399_M781}	----aaagttt	tagtagttga	tgatgaacca gttgcacgta acgaattaat
Consensus	***-----	-----	-----
	51		100
msa141507.2{399_A909}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_CJB110}	-----CTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_H36B}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_JM9130013}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_1169NT}	ttatcttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_090}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_18RS21}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_2603}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_COH1}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_M732}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
msa141507.2{399_M781}	ttaccttCTT	AATAAGTATG	ATTCTAACCT CGTTATAGCA GAGGCGCATG
Consensus	-----***	*****	*****
	101		150
msa141507.2{399_A909}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_CJB110}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_H36B}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_JM9130013}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_1169NT}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_090}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_18RS21}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_2603}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_COH1}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_M732}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
msa141507.2{399_M781}	ATATgGCTAC	TGCATTAGCT	ATTTTACTTA GAGAACTTT TGATGTAGCA
Consensus	*****	*****	*****
	151		200
msa141507.2{399_A909}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT GGGTTGCAAT TAGCAGAGTA
msa141507.2{399_CJB110}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT GGGTTGCAAT TAGCAGAGTA
msa141507.2{399_H36B}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT GGGTTGCAAT TAGCAGAGTA
msa141507.2{399_JM9130013}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT GGGTTGCAAT TAGCAGAGTA
msa141507.2{399_1169NT}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT GGGTTGCAAT TAGCAGAGTA

Table 78: Comparative Sequences relating to SAG1016

msa141507.2{399_090}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_18RS21}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_2603}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_COH1}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_M732}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_M781}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
Consensus	*****	*****	*****	*****	*****
msa141507.2{399_A909}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_CJB110}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_H36B}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_JM9130013}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_1169NT}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_090}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_18RS21}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_2603}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_COH1}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_M732}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_M781}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
Consensus	*****	*****	*****	*****-***	*****
msa141507.2{399_A909}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTGA
msa141507.2{399_CJB110}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTGA
msa141507.2{399_H36B}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTGA
msa141507.2{399_JM9130013}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTGA
msa141507.2{399_1169NT}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTGA
msa141507.2{399_090}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTGA
msa141507.2{399_18RS21}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTGA
msa141507.2{399_2603}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTGA
msa141507.2{399_COH1}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTGA
msa141507.2{399_M732}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTGA
msa141507.2{399_M781}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTGA
Consensus	*****	*****-***	*****-*	*****	*****
msa141507.2{399_A909}	AAACCCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_CJB110}	AAACCCCTATG	AgTTTGATAG	GcTAAAGCAA	GnTATGGATA	GAGTAAAGG
msa141507.2{399_H36B}	AAACCCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_JM9130013}	AAACCCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_1169NT}	AAACCCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_090}	AAACCCCTATG	AtTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_18RS21}	AAACCCCTATG	AtTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_2603}	AAACCCCTATG	AtTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_COH1}	AAACCCCTATG	AgTTTGATAG	GtTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_M732}	AAACCCCTATG	AgTTTGATAG	GtTAAAGCAA	GcTATGGATA	GAGTAAAGG
msa141507.2{399_M781}	AAACCCCTATG	AgTTTGATAG	GtTAAAGCAA	GcTATGGATA	GAGTAAAGG
Consensus	*****	*-*****	*-*****	*-*****	*****
msa141507.2{399_A909}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_CJB110}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_H36B}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_JM9130013}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_1169NT}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_090}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_18RS21}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_2603}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_COH1}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_M732}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_M781}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
Consensus	*****	*****	*****	*****	*****
msa141507.2{399_A909}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_CJB110}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATnGAATCTA	TCTGGTGTCTG
msa141507.2{399_H36B}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_JM9130013}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_1169NT}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_090}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_18RS21}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_2603}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_COH1}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_M732}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
msa141507.2{399_M781}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCTG
Consensus	*****	*****	*****	**-*****	*****
msa141507.2{399_A909}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_CJB110}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_H36B}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_JM9130013}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA

Table 78: Comparative Sequences relating to SAG1016

msa141507.2{399_1169NT}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_090}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_18RS21}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_2603}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_COH1}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_M732}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_M781}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
Consensus	*****	*****	*****	*****	*****
msa141507.2{399_A909}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_CJB110}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_H36B}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_JM9130013}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_1169NT}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_090}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_18RS21}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_2603}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_COH1}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_M732}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_M781}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
Consensus	*****	*****	*****	*****	*****
msa141507.2{399_A909}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCAcCGCTC	TTACATTGTG
msa141507.2{399_CJB110}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCAcCGCTC	TTACATTGTG
msa141507.2{399_H36B}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCAcCGCTC	TTACATTGTG
msa141507.2{399_JM9130013}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCAcCGCTC	TTACATTGTG
msa141507.2{399_1169NT}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCAcCGCTC	TTACATTGTG
msa141507.2{399_090}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_18RS21}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_2603}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_COH1}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_M732}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_M781}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
Consensus	*****	*****	*****	*_...*****	*****
msa141507.2{399_A909}	AAtATTAATG	CTATTAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_CJB110}	AAtATTAATG	CTATTAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_H36B}	AAtATTAATG	CTATTAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_JM9130013}	AAtATTAATG	CTATTAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_1169NT}	AAtATTAATG	CTATTAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_090}	AAtATTAATG	CTATTAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_18RS21}	AAtATTAATG	CTATTAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_2603}	AAtATTAATG	CTATTAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_COH1}	AAtATTAATG	CTATTAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_M732}	AAtATTAATG	CTATTAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_M781}	AAtATTAATG	CTATTAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
Consensus	**_*****	*****	*****	*****	*****
msa141507.2{399_A909}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_CJB110}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_H36B}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_JM9130013}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_1169NT}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_090}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_18RS21}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_2603}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_COH1}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_M732}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_M781}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
Consensus	*****	*****	*****	*****	*****
msa141507.2{399_A909}	AACCCCTAAA	ACAAATGTGA	GGcatatcta	cc	
msa141507.2{399_CJB110}	AACCCCTAAA	ACAAATGTGA	GG-----	--	
msa141507.2{399_H36B}	AACCCCTAAA	ACAAATGTGA	GGcatatcta	cc	
msa141507.2{399_JM9130013}	AACCCCTAAA	ACAAATGTGA	GGcatatcta	cc	
msa141507.2{399_1169NT}	AACCCCTAAA	ACAAATGTGA	GGcatatcta	cc	
msa141507.2{399_090}	AACCCCTAAA	ACAAATGTGA	GGcatatcta	cc	
msa141507.2{399_18RS21}	AACCCCTAAA	ACAAATGTGA	GGcatatcta	cc	
msa141507.2{399_2603}	AACCCCTAAA	ACAAATGTGA	GGcatatcta	cc	
msa141507.2{399_COH1}	AACCCCTAAA	ACAAATGTGA	GGcatatcta	cc	
msa141507.2{399_M732}	AACCCCTAAA	ACAAATGTGA	GGcatatcta	cc	
msa141507.2{399_M781}	AACCCCTAAA	ACAAATGTGA	GGcatatcta	cc	
Consensus	*****	*****	*****	---	

SEQ ID NO. 7812

STRAIN 2603 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALAILLRETFDVALLDIHLRDDSG
 LQLAEYINKMPKPLLIIFATAYDQYAIQAFEHDDARDYLLKPYDFDRLKQAMDRVKALST

Table 78: Comparative Sequences relating to SAG1016

STIIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7813

STRAIN 090 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETDFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7814

STRAIN A909 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETDFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7815

STRAIN H36B frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETDFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7816

STRAIN 18RS21 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETDFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7817

STRAIN M732 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETDFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVAGSGLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7818

STRAIN COH1 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETDFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVAGSGLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7819

STRAIN M781 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETDFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVAGSGLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7820

STRAIN CJB110 frame: 1

LNKYDSNLVIAEAHDMATALA ILLRETDFDVALLDIHLRDDSG LQLAEYINKMPKPPLLI F
ATAYDQYAI QAFEHDARDYLLKPYEFDRLKQXMDRVKGALSTSTIIESVTSGPLFKQQYP
LTVEDXIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQWQDKLPSSQFVRVHRSYI
VNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQML

SEQ ID NO. 7821

STRAIN 1169NT frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDIATALA ILLRETDFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7822

STRAIN JM9130013 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETDFDVALLDIHLRDDSG
LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIESVTSGPLFKQQYPLTVEDRIYLVSAADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

Table 78: Comparative Sequences relating to SAG1016

PRETTY of: /biotmp/msa141801.2{*} April 10, 2003 06:38 ..

	1				50
msa141801.2{399_COH1}	kvlvvddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_M732}	kvlvvddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_M781}	kvlvvddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_090}	kvlvvddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_18RS21}	kvlvvddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_2603}	kvlvvddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_A909}	kvlvvddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_H36B}	kvlvvddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_JM9130013}	kvlvvddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_1169NT}	kvlvvddepv	arneliy1LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL
msa141801.2{399_CJB110}	-----LN	KYDSNLVIAE	AHDmATALAI	LLRETFDVAL	
Consensus	-----	-----**	*****	***-*****	*****
	51				100
msa141801.2{399_COH1}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EqDARDYLLK
msa141801.2{399_M732}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EqDARDYLLK
msa141801.2{399_M781}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EqDARDYLLK
msa141801.2{399_090}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhdARDYLLK
msa141801.2{399_18RS21}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhdARDYLLK
msa141801.2{399_2603}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhdARDYLLK
msa141801.2{399_A909}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhdARDYLLK
msa141801.2{399_H36B}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhdARDYLLK
msa141801.2{399_JM9130013}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhdARDYLLK
msa141801.2{399_1169NT}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhdARDYLLK
msa141801.2{399_CJB110}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF	EhdARDYLLK
Consensus	*****	*****	*****	*****	*-*****
	101				150
msa141801.2{399_COH1}	PYeFDRLKQa	MDRVKGALST	STIIESVaSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_M732}	PYeFDRLKQa	MDRVKGALST	STIIESVaSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_M781}	PYeFDRLKQa	MDRVKGALST	STIIESVaSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_090}	PYdFDRLKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_18RS21}	PYdFDRLKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_2603}	PYdFDRLKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_A909}	PYeFDRLKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_H36B}	PYeFDRLKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_JM9130013}	PYeFDRLKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_1169NT}	PYeFDRLKQa	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDrIYLVSA
msa141801.2{399_CJB110}	PYeFDRLKQx	MDRVKGALST	STIIESVtSG	PLFKQQYPLT	VEDxIYLVSA
Consensus	**--*****-	*****	*****-	*****	***-*****
	151				200
msa141801.2{399_COH1}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_M732}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_M781}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_090}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_18RS21}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_2603}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_A909}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_H36B}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_JM9130013}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_1169NT}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
msa141801.2{399_CJB110}	DDILLIEAMQ	GKLIITQTPDK	NYEIDGSLQQ	WQDKLPSSQF	VRVHRSYIVN
Consensus	*****	*****	*****	*****	*****
	201				243
msa141801.2{399_COH1}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_M732}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_M781}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_090}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_18RS21}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_2603}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_A909}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_H36B}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_JM9130013}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_1169NT}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg	ist
msa141801.2{399_CJB110}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQML-	---
Consensus	*****	*****	*****	*****	---

Table 79: Comparative Sequences relating to SAG2150

SEQ ID NO. 7901

STRAIN 2603

ATGGGAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCCGGCACTCCCTTTTGAAGGG
 CGTGCCCTTTTGGACGTCAATCTGAAAATGAAGATGCTTCTATACCGCGTTTCATTGGG
 CACACAGGTTCTGGAAAATCACTATTATGCAACTTTTGAATGGTTTACATATTCTTACA
 AAAGGTGAGGTAATTTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAATC
 AAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCAGAAAGTCAGCTTTTGA
 GAGACAGTTTAAAGGATGTTGCTTTTGGACCACAAAATTTTGGTATTTCTCAGATTGAA
 GCTGAAAGGCTGGCTGAAGAAAATTAAGGTTAGTTGGTATCAGTGAGGATTTATTTCGAT
 AAAAAATCCATTTGAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTA
 GCGATGGAACCCAAAGTACTAGTACTGGATGAGCCACAGCTGGACTTGATCCTAAGGGA
 AGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAAGGAATGACTATCGTCTTA
 GTGACTCACTTAATGGACGATGTAGCGGATTATGCTGACTATGTGTATGTTTGAAGCA
 GGGAAAGTAACCTTATCAGGACAACCAAAACAGATTTTCAAGAAGTAGAATTTTAGAA
 AGTAACAATTAGGAGTTCCCAAAATCACCAGTTTGCTCAAAGACTATCTCATAAGGGA
 TTAATTTACCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7902

STRAIN 090

GGAAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCC
 GGCACCTCCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATCTGAAAATTTGA
 AGATGCTTCTATACCGCGTTTCATTGGGCACACAGGTTCTGGAAAATCAA
 CTATTATGCAACTTTTGAATGGTTTACATATTCTTACAAAAGGTGAGGTA
 ATTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAATCAA
 ATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCAGAAAGTCAGC
 TTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACCACAAAATTTT
 GGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAAATTAAGGTT
 AGTTGGTATCAGTGAGGATTTATTTCGATAAAAATCCATTGAACTTTCTG
 GAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGCGATGGAACCC
 AAAGTACTAGTACTGGATGAGCCACAGCTGGACTTGATCCTAAGGGAAG
 AAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAAGGAATGACTA
 TCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGACTAT
 GTGTATGTTTGAAGCAGGGGAAAGTAACCTTATCAGGACAACCAAAACA
 GATTTTCAAGAAGTAGAATCTTTAGAAAAGTAACAATTAGGAGTTCCCA
 AAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATTAAATTTACCT
 AGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7903

STRAIN A909

GGAAATTGAATTTAAAAATGTAAGTTATACCTATCAA
 GCCGGCACTCCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATCTGAAAAT
 TGAAGATGCTTCTATACCGCGTTTCATTGGGCACACAGGTTCTGGAAAAT
 CAACTATTATGCAACTTTTGAATGGTTTACATATTCTTACAAAAGGTGAG
 GTAATTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAAT
 CAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCAGAAAGTC
 AGCTTTTGAAGAGACAGTTTAAAGATGTTGCTTTTGGACCACAAAAT
 TTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAAATTAAG
 GTTAGTTGGTATCAGTGAGGATTTATTTCGATAAAAATCCATTGAACTTT
 CTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGCGATGGAA
 CCCAAAGTACTAGTACTAGATGAGCCACAGCTGGACTTGATCCTAAGGG
 AAGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAAGGAATGA
 CTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGAC
 TATGTGTATGTTTGAAGCAGGGGAAAGTAACCTTATCAGGACAACCAAA
 GCAGATTTTCAAGAAGTAGAATCTTTAGAAAAGTAACAATTAGGAGTTT
 CCAAAATCACCAGTTTGTCTCAAAGGCTATCTCATAAGGGATTAAATTTA
 CCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTAAGCATGG
 A

SEQ ID NO. 7904

STRAIN H36B

GGAAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATC
 TGAATAATTGAAGATGCTTCTATACCGCGTTTCATTGGGCACACAGGTTCT
 GGAAAATCACTATTATGCAACTTTTGAATGGTTTACATATTCTTACAAA
 AGGTGAGGTAATTTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACA
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGATGTTGCTTTTGGACC
 ACAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAAGGTTAGTTGGTATCAGTGAGGATTTATTTCGATAAAAATCCATT
 GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGC
 GATGGAACCCAAAGTACTAGTACTAGATGAGCCACAGCTGGACTTGATC
 CTAAGGGAAGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGCTGACTATGTGTATGTTTGAAGCAGGGGAAAGTAACCTTATCAGGAC
 AACCAAGCAGATTTTCAAGAAGTAGAATCTTTAGAAAAGTAACAATTA
 GGAGTTCCCAAAATCACCAGTTTGTCTCAAAGGCTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7905

STRAIN 18RS21

GGAAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATC

Table 79: Comparative Sequences relating to SAG2150

TGAAAATTGAAGATGCTTCCTATACCGCGTTCATTGGGCACACAGGTTCT
 GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCTACAAA
 AGGTGAGGTAATGTGCGATGATTTTCTATTAAAGCAGGGGACAAGAACA
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACC
 ACAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAAGTTAGTTGGTATCAGTGAGGATTATTTCGATAAAAATCCATT
 GAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
 CTAAGGAAGAAAAGAATTAAATGACTCTTTTAAAAATCTTCATAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGCTGACTATGTGTATGTTTGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
 GGAGTTCCCAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7906

STRAIN M732

GGAAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCTTTTGAAGGCGTGCCCTTTTGGACGTCAATC
 TGAAAATTGAAGATGTTTCTATACCGCGTTCATTGGGCACACAGGTTCT
 GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCTACAAA
 AGGTGAGGTAATGTGCGATGATTTTCTATTAAAGCAGGGGACAAGAACA
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACC
 ACAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAAGTTAGTTGGTATCAGTGAGGATTATTTCGATAAAAATCCATT
 GAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
 CTAAGGAAGAAAAGAATTAAATGACTCTTTTAAAAATCTTCATAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGCTGACTATGTGTATGTTTGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
 GGAGTTCCCAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7907

STRAIN COH1

GGAAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCC
 GGCATCCTCTTTGAAGGCGTGCCCTTTTGGACGTCAATCTGAAAATTGA
 AGATGTTTCTATACCGCGTTCATTGGGCACACAGGTTCTGGAAAATCAA
 CTATTATGCAACTTTTGAATGGTTTACATATTCTACAAAAGGTGAGGTA
 ATTGTGCGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAATCAA
 ATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCAGAAAGTCAGC
 TTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACCACAAAATTT
 GGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAATTAAGGTT
 AGTTGGTATCAGTGAGGATTATTTCGATAAAAATCCATTGAACTTTCTG
 GAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGCGATGGAACCC
 AAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGAAG
 AAAAGAATTAAATGACTCTTTTAAAAATCTTCATAAAAAGGAATGACTA
 TCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGACTAT
 GTGTATGTTTGAAGCAGGGAAAGTAACCTTATCAGGACAACCAAAACA
 GATTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTAGGAGTTCCCA
 AAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATTAAATTTACCT
 AGTTTACCAATTACTATTACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7908

STRAIN M781

GGAAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCTTTTGAAGGCGTGCCCTTTTGGACGTCAATC
 TGAAAATTGAAGATGTTTCTATACCGCGTTCATTGGGCACACAGGTTCT
 GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCTACAAA
 AGGTGAGGTAATGTGCGATGATTTTCTATTAAAGCAGGGGACAAGAACA
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTTAGTTTTCATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACC
 ACAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAAGTTAGTTGGTATCAGTGAGGATTATTTCGATAAAAATCCATT
 GAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
 CTAAGGAAGAAAAGAATTAAATGACTCTTTTAAAAATCTTCATAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGCTGACTATGTGTATGTTTGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTTCAAGAAGTAGAACTTTTAGAAAGTAAACAATTA
 GGAGTTCCCAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7909

STRAIN CJB110

GGAAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCTTTTGAAGGCGTGCCCTTTTGGACGTCAATC

Table 79: Comparative Sequences relating to SAG2150

TGAAAATTGAAGATGCTTCTATACCGCGTTTCATTGGGCACACAGGTTCT
 GGGAAATCAACTATTATGCACTTTTGAATGGTTTACATATTCTTACAAA
 AGGTGAGGTAATTTGTGATGATTTTCTATTAAAGCAGGGGACAAGAAC
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTAGTTTTCAATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACC
 ACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATT
 GAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGC
 GATGGAACCCAAAGTACTAGTACTGGATGAGCCACAGCTGGACTTGATC
 CTAAGGGAAGAAAAGAAATTAATGACTCTTTTAAAAATCTTCATAAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGTGACTATGTGTATGTTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTTCAAGAAGTAGAAGCTTTAGAAAAGTAAACAATTA
 GGAGTTCCCAAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATT
 AAATTTACCTAGTTTACCAATTACTATTACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7910

STRAIN 1169NT

GGAATTGAATTTAAAAATGTAA

GTATACCTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGAC
 GTCAATCTGAAAATTGAAGATGCTTCTATACCGCGTTTCATTGGGCACAC
 AGGTTCTGGAATAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCT
 CTACAAAAGGTGAGGTAATTTGTGATGATTTTCTATTAAAGCAGGGGAC
 AAGAACAAGAAATCAAATTTATAAGGCAAAAAGTTGGTTAGTTTTTCA
 ATTTCCAGAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTT
 TTGGACACACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCT
 GAAGAAAAAATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAA
 TCCATTTGAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTA
 TTTTAGCGATGGAACCCAAAGTACTAGTACTGGATGAGCCACAGCTGGA
 CTTGATCTTAAGGGAAGAAAAGAAATTAATGACTCTTTTAAAAATCTTCA
 TAAAAAAGGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAG
 CGGATTATGCTGACTATGTGTATGTTTAGAAGCAGGGAAAGTAACCTTA
 TCAGGACCAACCAAAACAGATTTTCAAGAAGTAGAAGCTTTAGAAAAGTAA
 ACAATTAGGAGTTCCCAAAATCACCAGTTTGTCTCAAAGACTATCTCATA
 AGGGATTAAATTTACCTAGTTTACCAATTACTATTACGAATTTGTGGAG
 GCTATTAAAGCATGGA

SEQ ID NO. 7911

STRAIN JM9130013

GGAATTGAATTTAAAAATGTAAAGTT

ATACCTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGACGTT
 AATCTGAAAATTGAAGATGCTTCTATACCGCATTTCATTGGGCACACAGG
 TTCTGGAATAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCTTA
 CAAAAGGTGAGGTAATTTGTGATGATTTTCTATTAAAGCAGGGGACAAG
 AACAAAGAAATCAAATTTATAAGGCAAAAAGTTGGTTAGTTTTTCAAT
 TCCAGAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTG
 GACCACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAA
 GAAAAATTAAGGTTAGTTGGTATTAGTGAGGATTTATTCGATAAAAAATCC
 ATTTGAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTT
 TAGCGATGGAACCCAAAGTACTAGTACTGGATGAGCCACAGCTGGACTT
 GATCTTAAGGGAAGAAAAGAAATTAATGACTCTTTTAAAAATCTTCATAA
 AAAAGGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGG
 ATTATGCTGACTATGTGTATGTTTAGAAGCAGGGAAAGTAACCTTATCA
 GGACAACCAAAACAGATTTTCAAGAAGTAGAAGCTTTAGAAAAGTAAACA
 ATTAGGAGTTCCCAAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGG
 GATTAAATTTACCTAGTTTACCAATTACTATTACGAATTTGTGGAGGCT
 ATTAAAGCATGGA

PRETTY of: /biotmp/msa238454.2{*} May 14, 2003 06:55 ..

	1		50
msa238454.2{401_A909}	---GGAATTG	AATTTAAAAA	TGTAAGTTAT
msa238454.2{401_H36B}	---GGAATTG	AATTTAAAAA	TGTAAGTTAT
msa238454.2{401_090}	---GGAATTG	AATTTAAAAA	TGTAAGTTAT
msa238454.2{401_1169NT}	---GGAATTG	AATTTAAAAA	TGTAAGTTAT
msa238454.2{401_18RS21}	---GGAATTG	AATTTAAAAA	TGTAAGTTAT
msa238454.2{401_2603}	atgGGAATTG	AATTTAAAAA	TGTAAGTTAT
msa238454.2{401_CJB110}	---GGAATTG	AATTTAAAAA	TGTAAGTTAT
msa238454.2{401_COH1}	---GGAATTG	AATTTAAAAA	TGTAAGTTAT
msa238454.2{401_M732}	---GGAATTG	AATTTAAAAA	TGTAAGTTAT
msa238454.2{401_M781}	---GGAATTG	AATTTAAAAA	TGTAAGTTAT
msa238454.2{401_JM9130013}	---GGAATTG	AATTTAAAAA	TGTAAGTTAT
Consensus	*****	*****	*****
	51		100
msa238454.2{401_A909}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTCAA
msa238454.2{401_H36B}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTCAA
msa238454.2{401_090}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTCAA
msa238454.2{401_1169NT}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTCAA
msa238454.2{401_18RS21}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTCAA
msa238454.2{401_2603}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTCAA
msa238454.2{401_CJB110}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTCAA

Table 79: Comparative Sequences relating to SAG2150

msa238454.2{401_COH1}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTcAA	TCTGAAAATT	GAAGATGtTT
msa238454.2{401_M732}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTcAA	TCTGAAAATT	GAAGATGtTT
msa238454.2{401_M781}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTcAA	TCTGAAAATT	GAAGATGtTT
msa238454.2{401_JM9130013}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTcAA	TCTGAAAATT	GAAGATGcTT
Consensus	*****	*****	*****_*	*****	*****_*
msa238454.2{401_A909}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_H36B}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_090}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_1169NT}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_18RS21}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_2603}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_CJB110}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_COH1}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_M732}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_M781}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_JM9130013}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_H36B}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_090}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_1169NT}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_18RS21}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_2603}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_CJB110}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_COH1}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_M732}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_M781}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
msa238454.2{401_JM9130013}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTCTGA
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_H36B}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_090}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_1169NT}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_18RS21}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_2603}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_CJB110}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_COH1}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_M732}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_M781}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_JM9130013}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGTAA
msa238454.2{401_H36B}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGTAA
msa238454.2{401_090}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGTAA
msa238454.2{401_1169NT}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGTAA
msa238454.2{401_18RS21}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGTAA
msa238454.2{401_2603}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGTAA
msa238454.2{401_CJB110}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGTAA
msa238454.2{401_COH1}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGTAA
msa238454.2{401_M732}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGTAA
msa238454.2{401_M781}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGTAA
msa238454.2{401_JM9130013}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTCA	GCTTTTGTAA
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_H36B}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_090}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_1169NT}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_18RS21}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_2603}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_CJB110}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_COH1}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_M732}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_M781}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_JM9130013}	GAGACAGTTT	TAAAgGATGT	TGCTTTTGA	CCACAAAATT	TTGGTATTTC
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAAG	TTAGTTGGTA
msa238454.2{401_H36B}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAAG	TTAGTTGGTA
msa238454.2{401_090}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAAG	TTAGTTGGTA
msa238454.2{401_1169NT}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAAG	TTAGTTGGTA
msa238454.2{401_18RS21}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAAG	TTAGTTGGTA
msa238454.2{401_2603}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAAG	TTAGTTGGTA

Table 79: Comparative Sequences relating to SAG2150

msa238454.2{401_CJB110}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_COH1}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_M732}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_M781}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_JM9130013}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_H36B}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_090}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_1169NT}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_18RS21}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_2603}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_CJB110}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_COH1}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_M732}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_M781}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_JM9130013}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
Consensus	*-*****	*****	*****	*****	*****
msa238454.2{401_A909}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_H36B}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_090}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_1169NT}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_18RS21}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_2603}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_CJB110}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_COH1}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_M732}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_M781}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_JM9130013}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	AGTACTaGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_H36B}	AGTACTaGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_090}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_1169NT}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_18RS21}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_2603}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_CJB110}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_COH1}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_M732}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_M781}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_JM9130013}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
Consensus	*****-***	*****	*****	*****	*****
msa238454.2{401_A909}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_H36B}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_090}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_1169NT}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_18RS21}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_2603}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_CJB110}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_COH1}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_M732}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_M781}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_JM9130013}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_H36B}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_090}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_1169NT}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_18RS21}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_2603}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_CJB110}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_COH1}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_M732}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_M781}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_JM9130013}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
Consensus	*****	*****	*****	*****	*****
msa238454.2{401_A909}	TTTGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAag	CAGATTTTTTC
msa238454.2{401_H36B}	TTTGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAag	CAGATTTTTTC
msa238454.2{401_090}	TTTGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAa	CAGATTTTTTC
msa238454.2{401_1169NT}	TTTGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAa	CAGATTTTTTC
msa238454.2{401_18RS21}	TTTGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAa	CAGATTTTTTC

Table 79: Comparative Sequences relating to SAG2150

msa238454.2{401_2603}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
msa238454.2{401_CJB110}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
msa238454.2{401_COH1}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
msa238454.2{401_M732}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
msa238454.2{401_M781}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
msa238454.2{401_JM9130013}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTC
Consensus	*****	*****	*****	*****	*****
701					
msa238454.2{401_A909}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_H36B}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_090}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_1169NT}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_18RS21}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_2603}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_CJB110}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_COH1}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_M732}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_M781}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_JM9130013}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
Consensus	*****	*****	*****	*****	*****
751					
msa238454.2{401_A909}	AAGTTTGCTC	AAAGgCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_H36B}	AAGTTTGCTC	AAAGgCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_090}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_1169NT}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_18RS21}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_2603}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_CJB110}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_COH1}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_M732}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_M781}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_JM9130013}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
Consensus	*****	*****	*****	*****	*****
801					
msa238454.2{401_A909}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_H36B}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_090}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_1169NT}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_18RS21}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_2603}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_CJB110}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_COH1}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_M732}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_M781}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_JM9130013}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
Consensus	*****	*****	*****	*****	
840					
SEQ ID NO. 7912					
STRAIN 2603 frame: 1					
MGIEFKNVSYTYQAGTFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK					
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFISQIEA					
ERLAEEKLRLVIGISEDLFDPKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR					
KELMTLFLKNLHKKGMTIVLVTHLMDVDVADYVYVLEAGKVTLSGQPKQIFQEVVELLES					
KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG					
SEQ ID NO. 7913					
STRAIN 090 frame: 1					
GIEFKNVSYTYQAGTFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK					
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFISQIEA					
ERLAEEKLRLVIGISEDLFDPKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR					
KELMTLFLKNLHKKGMTIVLVTHLMDVDVADYVYVLEAGKVTLSGQPKQIFQEVVELLES					
KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG					
SEQ ID NO. 7914					
STRAIN 090 frame: 1					
GIEFKNVSYTYQAGTFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK					
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFISQIEA					
ERLAEEKLRLVIGISEDLFDPKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR					
KELMTLFLKNLHKKGMTIVLVTHLMDVDVADYVYVLEAGKVTLSGQPKQIFQEVVELLES					
KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG					
SEQ ID NO. 7915					
STRAIN H36B frame: 1					
GIEFKNVSYTYQAGTFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK					
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFISQIEA					
ERLAEEKLRLVIGISEDLFDPKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR					
KELMTLFLKNLHKKGMTIVLVTHLMDVDVADYVYVLEAGKVTLSGQPKQIFQEVVELLES					
KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG					
SEQ ID NO. 7916					

Table 79: Comparative Sequences relating to SAG2150

STRAIN 18RS21 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTSGSKSTIMQLLNLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKPNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDYADYVYVLEAGKVTLSGQPKQIFQEVLELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7917

STRAIN M732 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTSGSKSTIMQLLNLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKPNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDYADYVYVLEAGKVTLSGQPKQIFQEVLELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7918

STRAIN COH1 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTSGSKSTIMQLLNLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKPNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDYADYVYVLEAGKVTLSGQPKQIFQEVLELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7919

STRAIN M781 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDVSYTAFIGHTSGSKSTIMQLLNLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKPNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDYADYVYVLEAGKVTLSGQPKQIFQEVLELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7920

STRAIN CJB110 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTSGSKSTIMQLLNLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKPNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDYADYVYVLEAGKVTLSGQPKQIFQEVLELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7921

STRAIN 1169NT frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTSGSKSTIMQLLNLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKPNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDYADYVYVLEAGKVTLSGQPKQIFQEVLELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

SEQ ID NO. 7922

STRAIN JM9130013 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTSGSKSTIMQLLNLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPQNFISQIEA
 ERLAEEKLRLVGISEDLDKPNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLTFKNLHKKGMTIVLVTHLMDDVDYADYVYVLEAGKVTLSGQPKQIFQEVLELLES
 KQLGVPKITKFAQRLSHKGLNLPISLPITINEFVEAIKHG

PRETTY of: /biotmp/msa238553.2{*} May 14, 2003 06:55 ..

	1		50
msa238553.2{401_090}	~GIEFKNVSY TYQAGTPFEG RALFDVNLKI	EDaSYTAFIG HTGSGKSTIM	
msa238553.2{401_1169NT}	~GIEFKNVSY TYQAGTPFEG RALFDVNLKI	EDaSYTAFIG HTGSGKSTIM	
msa238553.2{401_18RS21}	~GIEFKNVSY TYQAGTPFEG RALFDVNLKI	EDaSYTAFIG HTGSGKSTIM	
msa238553.2{401_2603}	mGIEFKNVSY TYQAGTPFEG RALFDVNLKI	EDaSYTAFIG HTGSGKSTIM	
msa238553.2{401_CJB110}	~GIEFKNVSY TYQAGTPFEG RALFDVNLKI	EDaSYTAFIG HTGSGKSTIM	
msa238553.2{401_H36B}	~GIEFKNVSY TYQAGTPFEG RALFDVNLKI	EDaSYTAFIG HTGSGKSTIM	
msa238553.2{401_JM9130013}	~GIEFKNVSY TYQAGTPFEG RALFDVNLKI	EDaSYTAFIG HTGSGKSTIM	
msa238553.2{401_COH1}	~GIEFKNVSY TYQAGTPFEG RALFDVNLKI	EDvSYTAFIG HTGSGKSTIM	
msa238553.2{401_M732}	~GIEFKNVSY TYQAGTPFEG RALFDVNLKI	EDvSYTAFIG HTGSGKSTIM	
msa238553.2{401_M781}	~GIEFKNVSY TYQAGTPFEG RALFDVNLKI	EDvSYTAFIG HTGSGKSTIM	
Consensus	*****	*****	***-*****
	51		100
msa238553.2{401_090}	QLLNLGLHIPT KGEVIVDDFS IKAGDKNKEI	KFIRQKVGLV FQFPESQLFE	
msa238553.2{401_1169NT}	QLLNLGLHIPT KGEVIVDDFS IKAGDKNKEI	KFIRQKVGLV FQFPESQLFE	
msa238553.2{401_18RS21}	QLLNLGLHIPT KGEVIVDDFS IKAGDKNKEI	KFIRQKVGLV FQFPESQLFE	
msa238553.2{401_2603}	QLLNLGLHIPT KGEVIVDDFS IKAGDKNKEI	KFIRQKVGLV FQFPESQLFE	
msa238553.2{401_CJB110}	QLLNLGLHIPT KGEVIVDDFS IKAGDKNKEI	KFIRQKVGLV FQFPESQLFE	
msa238553.2{401_H36B}	QLLNLGLHIPT KGEVIVDDFS IKAGDKNKEI	KFIRQKVGLV FQFPESQLFE	
msa238553.2{401_JM9130013}	QLLNLGLHIPT KGEVIVDDFS IKAGDKNKEI	KFIRQKVGLV FQFPESQLFE	
msa238553.2{401_COH1}	QLLNLGLHIPT KGEVIVDDFS IKAGDKNKEI	KFIRQKVGLV FQFPESQLFE	
msa238553.2{401_M732}	QLLNLGLHIPT KGEVIVDDFS IKAGDKNKEI	KFIRQKVGLV FQFPESQLFE	
msa238553.2{401_M781}	QLLNLGLHIPT KGEVIVDDFS IKAGDKNKEI	KFIRQKVGLV FQFPESQLFE	

Table 79: Comparative Sequences relating to SAG2150

Consensus	*****	*****	*****	*****	*****
	101				150
msa238553.2{401_090}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_1169NT}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_18RS21}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_2603}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_CJB110}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_H36B}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_JM9130013}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_COH1}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_M732}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_M781}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
Consensus	*****	*****	*****	*****	*****
	151				200
msa238553.2{401_090}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_1169NT}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_18RS21}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_2603}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_CJB110}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_H36B}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_JM9130013}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_COH1}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_M732}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
msa238553.2{401_M781}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIIVL
Consensus	*****	*****	*****	*****	*****
	201				250
msa238553.2{401_090}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_1169NT}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_18RS21}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_2603}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_CJB110}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_H36B}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_JM9130013}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_COH1}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_M732}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_M781}	VTHLMDDVAD	YADYVYVLEA	GKVTLSGQPK	QIFQEVLEL	SKQLGVPKIT
Consensus	*****	*****	*****	*****	*****
	251				280
msa238553.2{401_090}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_1169NT}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_18RS21}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_2603}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_CJB110}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_H36B}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_JM9130013}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_COH1}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_M732}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_M781}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
Consensus	*****	*****	*****		

Table 80: Comparative Sequences relating to SAG1266

SEQ ID NO. 8001

STRAIN 2603

GTGAACCACTTACTTAACCTCAGTAAAGAAAATATAGCTAAAATAGATTTTGACTTTCTT
 AATGAGGCACCTTAATGCAAAATATTCGTTTGAAAGAATTAGTAGATGAACATAAAATTTCA
 AAAGAACTGGACAGTAAAGGTTGGTCCAAAAAGACTCTCGAACGATAAAAATCTTGTAC
 GATGGCCTTATCAATAAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATCCAA
 GTCATTCCATTGCTAATGTACATGTACTACTGTTTTTAATACCAGAAAGGAGAAATCT
 AAAAATTATAGAAATACAACTACAGTGATTATGAAATGGAGTTAATCAATGAGGATAGG
 CAACAATTTTCAAAATATGAAACAGTTGATTTAGACCAATTGATACTTGTGTATATTTT
 AATATTGATGACTACATTTTCATCATATTTAACAATA

SEQ ID NO. 8002

STRAIN H36B

AACCACTTACTTAACCTCAGTAAAGAAAATATAGCT
 AAAATAGATTTTGACTTTCTTAATGAGGCACCTTAATGCAAAATATTCGTTT
 GAAAGAATTAGTAGATGAACATAAAATTTCAAAGAAGCTGGACAGTAAAG
 GTTGGTCCAAAAAGACTCTCGAACGATAAAAATCTTGTACGATGGCCTT
 ATCAATAAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATCCA
 AGTCATTCCATTGCTAATGTACATGTACTACTGTTTTTAATACCAGAAA
 GGGAGAATTCTAAAAATATAGAAATATACAACTACAGTGATTATGAAATG
 GAGTTAATCAATGAGGATAGGCAACAATTTTCAAAATATGAAACAGTTGA
 TTTAGACCAATTGATACTTGTGTATATTTTAATATTGATGACTACATTT
 CATCATATTTAACAATA

SEQ ID NO. 8003

STRAIN 18RS21

AACCACTTACTTAACCTCAGTAAAGAAAATATAG
 CTAAAAATAGATTTTGACTTTCTTAATGAGGCACCTTAATGCAAAATATTCGTT
 TTGAAAGAATTAGTAGATGAACATAAAATTTCAAAGAAGCTGGACAGTAA
 AGGTTGGTCCAAAAAGACTCTCGAACGATAAAAATCTTGTACGATGGCCT
 TTATCAATAAACATATAGTTTCCCTAGATCGTGCAGATTATAACATTATC
 CAAGTCATTCCATTGCTAATGTACATGTACTACTGTTTTTAATACCAGA
 AAGGGAGAATTCTAAAAATATAGAAATATACAACTACAGTGATTATGAAA
 TGGAGTTAATCAATGAGGATAGGCAACAATTTTCAAAATATGAAACAGTT
 GATTTAGACCAATTGATACTTGTGTATATTTTAATATTGATGACTACAT
 TTCATCATATTTAACAATA

PRETTY of: /biotmp/msa49308.2{*} February 19, 2003 07:45 ..

	1		50
msa49308.2{408_18RS21}	---AACCACCT	TACTTAACCT	CAGTAAAGAA AATATAGCTA AAATAGATT
msa49308.2{408_2603}	gtgAACCACCT	TACTTAACCT	CAGTAAAGAA AATATAGCTA AAATAGATT
msa49308.2{408_H36B}	---AACCACCT	TACTTAACCT	CAGTAAAGAA AATATAGCTA AAATAGATT
Consensus	*****	*****	*****
	51		100
msa49308.2{408_18RS21}	TGACTTTCTT	AATGAGGCAC	TTAATGCAAA TATTCGTTTG AAAGAATTAG
msa49308.2{408_2603}	TGACTTTCTT	AATGAGGCAC	TTAATGCAAA TATTCGTTTG AAAGAATTAG
msa49308.2{408_H36B}	TGACTTTCTT	AATGAGGCAC	TTAATGCAAA TATTCGTTTG AAAGAATTAG
Consensus	*****	*****	*****
	101		150
msa49308.2{408_18RS21}	TAGATGAACCT	AAAAATTTCA	AAAGAACTGG ACAGTAAAGG TTGGTCCAAA
msa49308.2{408_2603}	TAGATGAACCT	AAAAATTTCA	AAAGAACTGG ACAGTAAAGG TTGGTCCAAA
msa49308.2{408_H36B}	TAGATGAACCT	AAAAATTTCA	AAAGAACTGG ACAGTAAAGG TTGGTCCAAA
Consensus	*****	*****	*****
	151		200
msa49308.2{408_18RS21}	AAAGACTCTC	GAACGATAAA	AATCTTGTAC GATGGCCTTA TCAATAAACA
msa49308.2{408_2603}	AAAGACTCTC	GAACGATAAA	AATCTTGTAC GATGGCCTTA TCAATAAACA
msa49308.2{408_H36B}	AAAGACTCTC	GAACGATAAA	AATCTTGTAC GATGGCCTTA TCAATAAACA
Consensus	*****	*****	*****
	201		250
msa49308.2{408_18RS21}	TATAGTTTCC	CTAGATCGTG	CAGATTATAA CATTATCCAA GTCATTCCAT
msa49308.2{408_2603}	TATAGTTTCC	CTAGATCGTG	CAGATTATAA CATTATCCAA GTCATTCCAT
msa49308.2{408_H36B}	TATAGTTTCC	CTAGATCGTG	CAGATTATAA CATTATCCAA GTCATTCCAT
Consensus	*****	*****	*****
	251		300
msa49308.2{408_18RS21}	TTGCTAATGT	ACATGTACTA	CTGTTTTTAA TACCAGAAAG GGAGAATTCT
msa49308.2{408_2603}	TTGCTAATGT	ACATGTACTA	CTGTTTTTAA TACCAGAAAG GGAGAATTCT
msa49308.2{408_H36B}	TTGCTAATGT	ACATGTACTA	CTGTTTTTAA TACCAGAAAG GGAGAATTCT
Consensus	*****	*****	*****
	301		350
msa49308.2{408_18RS21}	AAAAATTATA	GAATATACAA	CTACAGTGAT TATGAAATGG AGTTAATCAA
msa49308.2{408_2603}	AAAAATTATA	GAATATACAA	CTACAGTGAT TATGAAATGG AGTTAATCAA
msa49308.2{408_H36B}	AAAAATTATA	GAATATACAA	CTACAGTGAT TATGAAATGG AGTTAATCAA
Consensus	*****	*****	*****

Table 80: Comparative Sequences relating to SAG1266

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351                                     400
msa49308.2{408_18RS21} TGAGGATAGG CAACAATTTT CAAAATATGA AACAGTTGAT TTAGACCAAT
msa49308.2{408_2603} TGAGGATAGG CAACAATTTT CAAAATATGA AACAGTTGAT TTAGACCAAT
msa49308.2{408_H36B} TGAGGATAGG CAACAATTTT CAAAATATGA AACAGTTGAT TTAGACCAAT
Consensus *****

401                                     450
msa49308.2{408_18RS21} TGATACTTGT TGATATTTT AATATTGATG ACTACATTTC ATCATATTTA
msa49308.2{408_2603} TGATACTTGT TGATATTTT AATATTGATG ACTACATTTC ATCATATTTA
msa49308.2{408_H36B} TGATACTTGT TGATATTTT AATATTGATG ACTACATTTC ATCATATTTA
Consensus *****

451
msa49308.2{408_18RS21} ACAATA
msa49308.2{408_2603} ACAATA
msa49308.2{408_H36B} ACAATA
Consensus *****

SEQ ID NO. 8004
STRAIN 2603 frame: 1
VNHLNLSKENIAKIDFDLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILY
DGLINKHIVSLDRADYNI IQVIPFANVHVLFLIPERENSKNYRIYNYSYEMELINEDR
QQFSKYETVDLDQLILVDIFNIDDISSYLTII

SEQ ID NO. 8005
STRAIN H36B frame: 1
NHLLNLSKENIAKIDFDLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILYD
GLINKHIVSLDRADYNI IQVIPFANVHVLFLIPERENSKNYRIYNYSYEMELINEDRQ
QQFSKYETVDLDQLILVDIFNIDDISSYLTII

SEQ ID NO. 8006
STRAIN 18RS21 frame: 1
NHLLNLSKENIAKIDFDLNEALNANIRLKELVDELKISKELDSKGWSKKDSRTIKILYD
GLINKHIVSLDRADYNI IQVIPFANVHVLFLIPERENSKNYRIYNYSYEMELINEDRQ
QQFSKYETVDLDQLILVDIFNIDDISSYLTII

PRETTY of: /biotmp/msa49418.2{*} February 19, 2003 07:47 ..

1                                     50
msa49418.2{408_18RS21} -NHLLNLSKE NIAKIDFDL NEALNANIRL KELVDELKIS KELDSKGWSK
msa49418.2{408_2603} vNHLLNLSKE NIAKIDFDL NEALNANIRL KELVDELKIS KELDSKGWSK
msa49418.2{408_H36B} -NHLLNLSKE NIAKIDFDL NEALNANIRL KELVDELKIS KELDSKGWSK
Consensus *****

51                                     100
msa49418.2{408_18RS21} KDSRTIKILY DGLINKHIVS LDRADYNI IQ VIPFANVHVL LFLIPERENS
msa49418.2{408_2603} KDSRTIKILY DGLINKHIVS LDRADYNI IQ VIPFANVHVL LFLIPERENS
msa49418.2{408_H36B} KDSRTIKILY DGLINKHIVS LDRADYNI IQ VIPFANVHVL LFLIPERENS
Consensus *****

101                                    150
msa49418.2{408_18RS21} KNYRIYNYS YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDISSYL
msa49418.2{408_2603} KNYRIYNYS YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDISSYL
msa49418.2{408_H36B} KNYRIYNYS YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDISSYL
Consensus *****

151
msa49418.2{408_18RS21} TI
msa49418.2{408_2603} TI
msa49418.2{408_H36B} TI
Consensus **

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Table 81: Comparative Sequences relating to SAG0011

SEQ ID NO. 8101

STRAIN 090

AGCAAGCCTAATGTTGTTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATG
 CTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTTT
 ACAAGAACGTCGTCAGAAAGTTGTAAAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCAGAAGTTGCTAGCAAAACAATAAAAAAT
 CCAGATTACGTTCAAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
 CGCGAAATGATTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8102

STRAIN A909

AGCAAGCCTAATGTTGTTTCAGTTAAATAATCAATA
 TATTAAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGGAGTTACGCCGAAAAAATCG
 TTTAATGGGTTGGGTTCTTATTTTGTCTATGCTtttATTTATTTTACCCACTTATAATTT
 AGTTAAGAGTTACAGAACCTTTACAAGAACGTCGTCAGAAAGTTGTAAAAATTAACGAAAGA
 CTATCAGACATTAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAAA
 TCCAGATTACGTTCAAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGACCGCGAAAT
 GATTTACCCATTACCAGACCT

SEQ ID NO. 8103

STRAIN H36B

AGCAAGCCTAATGTTGTTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATG
 CTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTTT
 ACAAGAACGTCGTCAGAAAGTTGTAAAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAAAT
 CCAGATTACGTTCAAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
 CGCGAAATGATTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8104

STRAIN 18RS21

AGCAAGCCTAATGTTGTTTCAGTTAAATAATCAATATATTAACGATGAGAATCTAAAAA
 CGTTACGAAGCTGAGGAGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTT
 GTCATGCTTTTATTTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTTACAA
 GAACGTCGTCAGAAAGTTGTAAAAATTAACGAAAGACTATCAGACATTAACTAATAGAACT
 GAGAACCAGAAGTTGCTAGCAAAACAATAAAAAATCCAGATTACGTTCAAAAAATATGCT
 CGAGCTAAGTATTATTTCTCTAAGACCGCGAAATGATTTACCCATTACCAGACCTTTTA
 CCAAAA

SEQ ID NO. 8105

STRAIN M732

AGCAAGCCTAATGTTGTTTCAGTTAAA
 TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATG
 CTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTTT
 ACAAGAACGTCGTCAGAAAGTTGTAAAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAAAT
 CCAGATTACGTTCAAAAAATATGCTCGAGCGAAGTATTATTTCTCTAAGAC
 CGCGAAATGATTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8106

STRAIN COH1

AGCAAGCCTAATGTTGTTTCAGTTAAATAATC
 AATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGGAGTTA
 CGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATGCTttt
 ATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTTTACAAG
 AACGTCGTCAGAAAGTTGTAAAAATTAACGAAAGACTATCAGACATTAACT
 AATAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAAATCCAGA
 TTACGTTCAAAAAATATGCTCGAGCGAAGTATTATTTCTCTAAGACCGGCG
 AATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8107

STRAIN M781

AGCaAGCCTAATGTTGTTTCAGTT
 AAATAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTG
 AGGAGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATGCT
 ATGCTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAAC
 TTTACAAGAACGTCGTCAGAAAGTTGTAAAAATTAACGAAAGACTATCAGA
 CATTAACTAATAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAA
 AATCCAGATTACGTTCAAAAAATATGCTCGAGCGAAGTATTATTTCTCTA
 GACCGCGAAATGATTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8108

STRAIN CJB110

AGCAAGCCTAATGTTGTTTCAGTTAAATAATC
 AATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGGAGTTA
 CGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATGCTttt
 ATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTTTACAAG

Table 81: Comparative Sequences relating to SAG0011

AACGTCGTCAGAAGTTGTAAATTAACGAAAGACTATCAGACATTAAC
 AATAGAAGTGAAGACCAGAAGTTGCTAGCAAAACAACTAAAAATCCAGA
 TTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGACCGGCG
 AAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8109

STRAIN 1169NT

AGCAAGCCTAATGTTTTCAGTTAAA
 TAATCAATATATTAAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATG
 CTTTTATTTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTT
 ACAAGAAGCTCGTCAAGAAGTTGTAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAAGTGAAGACCAGAAGTTACTAGCAAAACAACTAAAAAT
 CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
 CGCGAAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8110

STRAIN JM9130013

AGCAAGCCTAATGTTTTCAGTTAAA
 TAATCAATATATTAAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
 AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATG
 CTTTTATTTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTT
 ACAAGAAGCTCGTCAAGAAGTTGTAAATTAACGAAAGACTATCAGACAT
 TAACTAATAGAAGTGAAGACCAGAAGTTACTAGCAAAACAACTAAAAAT
 CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
 TGGCGAAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8111

STRAIN 2603

agcaagcctaagtgtgttcagttaataatcaatatattaacgatgagaa
 tctaaaaaacggttacgaagctgaggagttacgccgaaaaaatcgtttaa
 tgggttgggttcttattttgtcatgcttttatttttaccacttat
 aatttagttaagagttacagaactttacaagaacgtcgtcaagaagttgt
 aaaattaacgaagactatcagacattaactaatagaactgagaaccaga
 agttgctagcaaaacaactaaaaatccagattacgttcaaaaatgatgct
 cgagctaagattattttctctaagaccggcgaaatgatttaccattacc
 agaccttttaccaaaa

PRETTY of: /biotmp/msa25643.2{*} . April 29, 2002 05:59 ..

	1		50
msa25643.2{418_COH1}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_M732}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_M781}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_JM9130013}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_090}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_18RS21}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_2603}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_CJB110}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_1169NT}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_A909}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
msa25643.2{418_H36B}	AGCAAGCCTA	ATGTTGTTCA	GTTAAATAAT CAATATATTA ACGATGAGAA
Consensus	*****	*****	*****
	51		100
msa25643.2{418_COH1}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_M732}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_M781}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_JM9130013}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_090}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_18RS21}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_2603}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_CJB110}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_1169NT}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_A909}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
msa25643.2{418_H36B}	TCTAAAAAAA	CGTTACGAAG	CTGAGGAGTT ACGCCGAAAA AATCGTTTAA
Consensus	*****	*****	*****
	101		150
msa25643.2{418_COH1}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_M732}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_M781}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_JM9130013}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_090}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_18RS21}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_2603}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_CJB110}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_1169NT}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_A909}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
msa25643.2{418_H36B}	TGGGTTGGGT	TCCTATTTT	GTCATGCTTT TATTTATTTT ACCCACTTAT
Consensus	*****	*****	*****

Table 81: Comparative Sequences relating to SAG0011

		151			200	
msa25643.2{418_COH1}		AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_M732}		AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_M781}		AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_JM9130013}		AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_090}		AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_18RS21}		AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_2603}		AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_CJB110}		AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_1169NT}		AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_A909}		AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_H36B}		AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
Consensus		*****	*****	*****	*****	*****
		201			250	
msa25643.2{418_COH1}		AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_M732}		AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_M781}		AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_JM9130013}		AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_090}		AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_18RS21}		AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_2603}		AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_CJB110}		AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_1169NT}		AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_A909}		AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_H36B}		AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
Consensus		*****	*****	*****	*****	*****
		251			300	
msa25643.2{418_COH1}		AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_M732}		AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_M781}		AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_JM9130013}		AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_090}		AGTTgCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_18RS21}		AGTTgCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_2603}		AGTTgCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_CJB110}		AGTTgCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_1169NT}		AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_A909}		AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_H36B}		AGTTaCTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
Consensus		****-*****	*****	*****	*****	*****
		301			350	
msa25643.2{418_COH1}		CGAGCgAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_M732}		CGAGCgAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_M781}		CGAGCgAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_JM9130013}		CGAGCgAAGT	ATTATTTCTC	TAAGACtGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_090}		CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_18RS21}		CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_2603}		CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_CJB110}		CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_1169NT}		CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_A909}		CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_H36B}		CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
Consensus		*****-****	*****	*****-***	*****	*****
		351	366			
msa25643.2{418_COH1}		AGACCTTttaa	ccaaaa			
msa25643.2{418_M732}		AGACCTTttaa	ccaaaa			
msa25643.2{418_M781}		AGACCTTttaa	ccaaaa			
msa25643.2{418_JM9130013}		AGACCTTttaa	ccaaaa			
msa25643.2{418_090}		AGACCTTttaa	ccaaaa			
msa25643.2{418_18RS21}		AGACCTTttaa	ccaaaa			
msa25643.2{418_2603}		AGACCTTttaa	ccaaaa			
msa25643.2{418_CJB110}		AGACCTTttaa	ccaaaa			
msa25643.2{418_1169NT}		AGACCTTttaa	ccaaaa			
msa25643.2{418_A909}		AGACCT-----	-----			
msa25643.2{418_H36B}		AGACCTTttaa	ccaaaa			
Consensus		*****-----	-----			

SEQ ID NO. 8112

STRAIN 090

SKPNVQVLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
VKSRYRTLQERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFSKTGEM
IYPLDLLPK

SEQ ID NO. 8113

STRAIN A909

SKPNVQVLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
VKSRYRTLQERRQEVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFSKTGEM

Table 81: Comparative Sequences relating to SAG0011

IYPLPD

SEQ ID NO. 8114

STRAIN H36B

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8115

STRAIN 18RS21

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVKSYRTLQ
 ERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM IYPLPDLL
 PK

SEQ ID NO. 8116

STRAIN M732

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8117

STRAIN COH1

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVK
 SYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM IY
 PLPDLLPK

SEQ ID NO. 8118

STRAIN M781

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 LVKSYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGE
 MIYPLPDLLPK

SEQ ID NO. 8119

STRAIN CJB110

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVK
 SYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM IY
 PLPDLLPK

SEQ ID NO. 8120

STRAIN 1169NT

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8121

STRAIN JM9130013

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8122

STRAIN 2603

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVKSYRTLQ
 ERRQEVVVKLT KDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM IYPLPDLL
 PK

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa20122.2{*} April 29, 2002 06:08 ..

	1		50
msa20122.2{418_090}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK NRLMGWVLIF	VMLLFILPTY
msa20122.2{418_A909}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK NRLMGWVLIF	VMLLFILPTY
msa20122.2{418_1169NT}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK NRLMGWVLIF	VMLLFILPTY
msa20122.2{418_18RS21}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK NRLMGWVLIF	VMLLFILPTY
msa20122.2{418_2603}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK NRLMGWVLIF	VMLLFILPTY
msa20122.2{418_CJB110}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK NRLMGWVLIF	VMLLFILPTY
msa20122.2{418_COH1}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK NRLMGWVLIF	VMLLFILPTY
msa20122.2{418_H36B}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK NRLMGWVLIF	VMLLFILPTY
msa20122.2{418_JM9130013}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK NRLMGWVLIF	VMLLFILPTY
msa20122.2{418_M732}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK NRLMGWVLIF	VMLLFILPTY
msa20122.2{418_M781}	SKPNVVQLNN	QYINDENLKK RYEAEELRRK NRLMGWVLIF	VMLLFILPTY
Consensus	*****	*****	*****
	51		100
msa20122.2{418_090}	NLVKSRYRTLQ	ERRQEVVVKLT KDYQTLTNRT	ENQKLLAKQL KNPDYVQKYA
msa20122.2{418_A909}	NLVKSRYRTLQ	ERRQEVVVKLT KDYQTLTNRT	ENQKLLAKQL KNPDYVQKYA

Table 81: Comparative Sequences relating to SAG0011

msa20122.2{418_1169NT}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_18RS21}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_2603}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_CJB110}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_COH1}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_H36B}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_JM9130013}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_M732}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_M781}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
Consensus	*****	*****	*****	*****	*****

	101	122
msa20122.2{418_090}	RAKYFSGKTG	EMIYPLPD11 pk
msa20122.2{418_A909}	RAKYFSGKTG	EMIYPLPD-- --
msa20122.2{418_1169NT}	RAKYFSGKTG	EMIYPLPD11 pk
msa20122.2{418_18RS21}	RAKYFSGKTG	EMIYPLPD11 pk
msa20122.2{418_2603}	RAKYFSGKTG	EMIYPLPD11 pk
msa20122.2{418_CJB110}	RAKYFSGKTG	EMIYPLPD11 pk
msa20122.2{418_COH1}	RAKYFSGKTG	EMIYPLPD11 pk
msa20122.2{418_H36B}	RAKYFSGKTG	EMIYPLPD11 pk
msa20122.2{418_JM9130013}	RAKYFSGKTG	EMIYPLPD11 pk
msa20122.2{418_M732}	RAKYFSGKTG	EMIYPLPD11 pk
msa20122.2{418_M781}	RAKYFSGKTG	EMIYPLPD11 pk
Consensus	*****	*****-- --

Table 82: Comparative Sequences relating to SAG0165

SEQ ID NO. 8201

STRAIN 2603

ATGAAAAATTATTGTTAAAAATGTAAGGATAAGAAGGTTAAAGCATTTACACTTTTAGAA
 TGTTTGGTAGCATTGGTTACAATCACAGGAGCTTTACTAGTTTATCAAGGACTGACAAAA
 TTGTTGGCTCAACAGATAGTAGTGATGCTTCTCCAGTCAGTCTGAATGGGTGTTATTA
 AcTCAGCAACTAAATGCAGAATTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAA
 CTTTATTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATTC
 CGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGTTAGACAATTGT
 CAAATGAGTCAGACCAAAAGTATGGTAAAACTTGT'TTTTATTTAAGGACGGGTAAAA
 AGGACATTTTACTATGATTTTAAAGAAGAACTTAA

SEQ ID NO. 8202

STRAIN 090

AATTCGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTATTTA
 CGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATT
 CCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGT
 TAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACTTGT'TTTT
 TATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAGA
 AACT

SEQ ID NO. 8203

STRAIN A909

CAGAATTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTTTAT
 TTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGA
 TTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATG
 GGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGT'T
 TTTTATTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGA
 AGAAACT

SEQ ID NO. 8204

STRAIN H36B

ATGCAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTT
 TATTTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGA
 TGATTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTT
 ATGGGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTT
 GTTTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAA
 AGAAGAACT

SEQ ID NO. 8205

STRAIN 18RS21

AGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTTTATT
 TACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
 TTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGG
 GTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGT'TT
 TTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAA
 GAACT

SEQ ID NO. 8206

STRAIN M732

CAGAATTGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTAT
 TTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGA
 TTTCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTTATG
 GGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGT'T
 TTTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGA
 AGAACT

SEQ ID NO. 8207

STRAIN COH1

GAATTCGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTATTT
 ACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATT
 TCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTTATGGG
 TTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGT'TTT
 TTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAG
 AACT

SEQ ID NO. 8208

STRAIN M781

AGAATTCGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTATT
 TACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
 TTCCGTAAGACAGGTTATAATGGTCGAGGTTATCAACCAATGGTTTATGG
 GTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAAACTTGT'TT
 TTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAA
 GAACT

SEQ ID NO. 8209

STRAIN CJB110

GAATTCGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTATTT
 ACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATT
 TCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGG
 TTAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACTTGT'TTT
 TTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAG
 AACT

Table 82: Comparative Sequences relating to SAG0165

SEQ ID NO. 8210

STRAIN 1169NT

TCGAAGGCGCTCACTTGGAAATATTTAAGACAGAACAACTTTATTACGT
 AAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAGATGATTTTCG
 TAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGTTAG
 ACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAACTTGTTTTAT
 TTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAGAAAC
 T

SEQ ID NO. 8211

STRAIN JM9130013

TGCAGAAITTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTTT
 ATTTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAGAT
 GATTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTA
 TGGGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATGGTAAACTTG
 TTTTATTTTAAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAA
 GAAGAACT

PRETTY of: /biotmp/msa128189.2{*} February 7, 2003 08:19 ..

	1				50
msa128189.2{6_18RS21}	-----	-----	-----	-----	-----
msa128189.2{6_2603}	atgaaaaatt	tattgttaaa	atgtaaggat	aagaaggtta	aagcatttac
msa128189.2{6_A909}	-----	-----	-----	-----	-----
msa128189.2{6_H36B}	-----	-----	-----	-----	-----
msa128189.2{6_JM9130013}	-----	-----	-----	-----	-----
msa128189.2{6_COH1}	-----	-----	-----	-----	-----
msa128189.2{6_M732}	-----	-----	-----	-----	-----
msa128189.2{6_M781}	-----	-----	-----	-----	-----
msa128189.2{6_090}	-----	-----	-----	-----	-----
msa128189.2{6_CJB110}	-----	-----	-----	-----	-----
msa128189.2{6_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa128189.2{6_18RS21}	-----	-----	-----	-----	-----
msa128189.2{6_2603}	acttttagaa	tggttgtag	cattgggtac	aatcacagga	gctttactag
msa128189.2{6_A909}	-----	-----	-----	-----	-----
msa128189.2{6_H36B}	-----	-----	-----	-----	-----
msa128189.2{6_JM9130013}	-----	-----	-----	-----	-----
msa128189.2{6_COH1}	-----	-----	-----	-----	-----
msa128189.2{6_M732}	-----	-----	-----	-----	-----
msa128189.2{6_M781}	-----	-----	-----	-----	-----
msa128189.2{6_090}	-----	-----	-----	-----	-----
msa128189.2{6_CJB110}	-----	-----	-----	-----	-----
msa128189.2{6_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	101				150
msa128189.2{6_18RS21}	-----	-----	-----	-----	-----
msa128189.2{6_2603}	tttatcaagg	actgacaaaa	ttgttggtc	aacagatagt	agtgatgtct
msa128189.2{6_A909}	-----	-----	-----	-----	-----
msa128189.2{6_H36B}	-----	-----	-----	-----	-----
msa128189.2{6_JM9130013}	-----	-----	-----	-----	-----
msa128189.2{6_COH1}	-----	-----	-----	-----	-----
msa128189.2{6_M732}	-----	-----	-----	-----	-----
msa128189.2{6_M781}	-----	-----	-----	-----	-----
msa128189.2{6_090}	-----	-----	-----	-----	-----
msa128189.2{6_CJB110}	-----	-----	-----	-----	-----
msa128189.2{6_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	151				200
msa128189.2{6_18RS21}	-----	-----	-----	-----	-----aga
msa128189.2{6_2603}	tcttccagtc	agtctgaatg	ggtgttatta	actcagcaac	taaATGCaga
msa128189.2{6_A909}	-----	-----	-----	-----	-----Caga
msa128189.2{6_H36B}	-----	-----	-----	-----	-----ATGCaga
msa128189.2{6_JM9130013}	-----	-----	-----	-----	-----TGCaga
msa128189.2{6_COH1}	-----	-----	-----	-----	-----ga
msa128189.2{6_M732}	-----	-----	-----	-----	-----Caga
msa128189.2{6_M781}	-----	-----	-----	-----	-----aga
msa128189.2{6_090}	-----	-----	-----	-----	-----a
msa128189.2{6_CJB110}	-----	-----	-----	-----	-----ga
msa128189.2{6_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****--
	201				250
msa128189.2{6_18RS21}	atTtGAAGGC	GCTCAtcTGG	AATATTTAAG	ACAGAACAAA	CITTTATTAC
msa128189.2{6_2603}	atTtGAAGGC	GCTCAtcTGG	AATATTTAAG	ACAGAACAAA	CITTTATTAC
msa128189.2{6_A909}	atTtGAAGGC	GCTCAtcTGG	AATATTTAAG	ACAGAACAAA	CITTTATTAC
msa128189.2{6_H36B}	atTtGAAGGC	GCTCAtcTGG	AATATTTAAG	ACAGAACAAA	CITTTATTAC

Table 82: Comparative Sequences relating to SAG0165

msa128189.2{6_JM9130013}	atTtGAAGGC	GCTCAtcTGG	AATATTTTAAg	ACAGAACAAA	CTTTATTtAC
msa128189.2{6_COH1}	atTcGAAGGC	GCTCActTGG	AATATTTTAAg	ACAGAACAAA	CTTTATTtAC
msa128189.2{6_M732}	atTcGAAGGC	GCTCActTGG	AATATTTTAAg	ACAGAACAAA	CTTTATTtAC
msa128189.2{6_M781}	atTcGAAGGC	GCTCActTGG	AATATTTTAAg	ACAGAACAAA	CTTTATTtAC
msa128189.2{6_090}	atTcGAAGGC	GCTCActTGG	AATATTTTAAg	ACAGAACAAA	CTTTATTtAC
msa128189.2{6_CJB110}	atTcGAAGGC	GCTCActTGG	AATATTTTAAg	ACAGAACAAA	CTTTATTtAC
msa128189.2{6_1169NT}	~TcGAAGGC	GCTCActTGG	AATATTTTAAg	ACAGAACAAA	CTTTATTtAC
Consensus	--*~*****	*****--***	*****	*****	*****
251					
msa128189.2{6_18RS21}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTtC
msa128189.2{6_2603}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTtC
msa128189.2{6_A909}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTtC
msa128189.2{6_H36B}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTtC
msa128189.2{6_JM9130013}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTtC
msa128189.2{6_COH1}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTtC
msa128189.2{6_M732}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTtC
msa128189.2{6_M781}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTtC
msa128189.2{6_090}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTtC
msa128189.2{6_CJB110}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTtC
msa128189.2{6_1169NT}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTtC
Consensus	*****	*****	*****	*****	*****
301					
msa128189.2{6_18RS21}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_2603}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_A909}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_H36B}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_JM9130013}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_COH1}	CGTAAGACAG	GTTATaATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_M732}	CGTAAGACAG	GTTATaATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_M781}	CGTAAGACAG	GTTATaATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_090}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_CJB110}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_1169NT}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
Consensus	*****	*****	*****	*****	*****
350					
msa128189.2{6_18RS21}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_2603}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_A909}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_H36B}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_JM9130013}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_COH1}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_M732}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_M781}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_090}	AGACAATTGT	CAAATGAGTC	AaACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_CJB110}	AGACAATTGT	CAAATGAGTC	AaACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_1169NT}	AGACAATTGT	CAAATGAGTC	AaACCAAAAG	TATGGTAAAA	CTTGTTTTTT
Consensus	*****	*****	*~*****	*****	*****
400					
msa128189.2{6_18RS21}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_2603}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_A909}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_H36B}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_JM9130013}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_COH1}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_M732}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_M781}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_090}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_CJB110}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_1169NT}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
Consensus	*****	*****	*****	*****	*****
451					
msa128189.2{6_18RS21}	ACT---				
msa128189.2{6_2603}	ACTtaa				
msa128189.2{6_A909}	ACT---				
msa128189.2{6_H36B}	ACT---				
msa128189.2{6_JM9130013}	ACT---				
msa128189.2{6_COH1}	ACT---				
msa128189.2{6_M732}	ACT---				
msa128189.2{6_M781}	ACT---				
msa128189.2{6_090}	ACT---				
msa128189.2{6_CJB110}	ACT---				
msa128189.2{6_1169NT}	ACT---				
Consensus	*****				

SEQ ID NO. 8212

STRAIN 2603 frame: 1

MKNLLKCKDKKVKAFLLLECLVALVTITGALLVYQGLTKLLAQQIVVMSSSSQSEWVLL
 TQQLNAEFEGAHLEYLRQNKLLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNC

Table 82: Comparative Sequences relating to SAG0165

QMSQTKSMVKLVFYFKDGLKRTFFYDFKEET.

SEQ ID NO. 8213

STRAIN 090 frame: 3

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTKS
MVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8214

STRAIN A909 frame: 3

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8215

STRAIN H36B frame: 3

AEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQT
KSMVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8216

STRAIN 18RS21 frame: 2

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8217

STRAIN M732 frame: 3

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8218

STRAIN COH1 frame: 1

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8219

STRAIN M781 frame: 2

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8220

STRAIN CJB110 frame: 1

EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8221

STRAIN 1169NT frame: 3

EGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTKSM
VKLVFYFKDGLKRTFFYDFKEET

SEQ ID NO. 8222

STRAIN JM9130013 frame: 2

AEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQT
KSMVKLVFYFKDGLKRTFFYDFKEET

PRETTY of: /biotmp/msa128319.2{*} February 7, 2003 08:27 ..

	1				50
msa128319.2{6_090}	-----	-----	-----	-----	-----
msa128319.2{6_1169NT}	-----	-----	-----	-----	-----
msa128319.2{6_18RS21}	-----	-----	-----	-----	-----
msa128319.2{6_2603}	mknlllkckd	kkvkaftlle	clvalvtitg	allvyqgltk	llaqqivvms
msa128319.2{6_H36B}	-----	-----	-----	-----	-----
msa128319.2{6_JM9130013}	-----	-----	-----	-----	-----
msa128319.2{6_A909}	-----	-----	-----	-----	-----
msa128319.2{6_CJB110}	-----	-----	-----	-----	-----
msa128319.2{6_COH1}	-----	-----	-----	-----	-----
msa128319.2{6_M732}	-----	-----	-----	-----	-----
msa128319.2{6_M781}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa128319.2{6_090}	-----	-----fEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_1169NT}	-----	-----EG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_18RS21}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_2603}	sssqsewvll	tqqlnAEfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_H36B}	-----	-----AEfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_JM9130013}	-----	-----AEfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_A909}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_CJB110}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_COH1}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_M732}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
msa128319.2{6_M781}	-----	-----EfEG	AHLEYLRQNK	LYLRKQDKIV	TFGKSNKDDF
Consensus	*****	*****-*	*****	*****	*****

Table 82: Comparative Sequences relating to SAG0165

	101		150
msa128319.2{6_090}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK LVFYFKDGLK RTFYDFKKEE
msa128319.2{6_1169NT}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK LVFYFKDGLK RTFYDFKKEE
msa128319.2{6_18RS21}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK LVFYFKDGLK RTFYDFKKEE
msa128319.2{6_2603}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK LVFYFKDGLK RTFYDFKKEE
msa128319.2{6_H36B}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK LVFYFKDGLK RTFYDFKKEE
msa128319.2{6_JM9130013}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK LVFYFKDGLK RTFYDFKKEE
msa128319.2{6_A909}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK LVFYFKDGLK RTFYDFKKEE
msa128319.2{6_CJB110}	RKTGYdGRGY	QPMVYGLDNC	QMSQTKSMVK LVFYFKDGLK RTFYDFKKEE
msa128319.2{6_COH1}	RKTGYnGRGY	QPMVYGLDNC	QMSQTKSMVK LVFYFKDGLK RTFYDFKKEE
msa128319.2{6_M732}	RKTGYnGRGY	QPMVYGLDNC	QMSQTKSMVK LVFYFKDGLK RTFYDFKKEE
msa128319.2{6_M781}	RKTGYnGRGY	QPMVYGLDNC	QMSQTKSMVK LVFYFKDGLK RTFYDFKKEE
Consensus	*****	*****	*****
	151		
msa128319.2{6_090}	T~		
msa128319.2{6_1169NT}	T~		
msa128319.2{6_18RS21}	T~		
msa128319.2{6_2603}	T~		
msa128319.2{6_H36B}	T~		
msa128319.2{6_JM9130013}	T~		
msa128319.2{6_A909}	T~		
msa128319.2{6_CJB110}	T~		
msa128319.2{6_COH1}	T~		
msa128319.2{6_M732}	T~		
msa128319.2{6_M781}	T~		
Consensus	**		

Table 83: Comparative Sequences relating to SAG0108

SEQ ID NO. 8301

STRAIN 2603

atgaaaaagattcgattatcaaagtttattaaaatgattgttgttattttgtttttaatt
 agtgtagcagctagtttttatttttccacgttgcccaagttcgagatgataaatccttt
 atttcaaatgggtcaacgttaagcctggaaactctttatatgtctatgataaatcctttgat
 aagctattaaagcaaaaaatagaaatgacaaacaaaataaaagcaagttgcttggat
 gttcctgctgttaagaaaactcataagacagctgttgcgttcaggttttgcgaatagc
 aaagagaatatgaaggcatatgggttggctgtttcataagttaggatataaatgttcttatg
 cctgacaatattgcacatgggtgaaagtcatgggcagttgataggctatggctggaacgac
 cgcgagaacattatcaaatggacagaaatgatagttgataagaatccatcaagccaaatt
 actttatttgggtgtttcaatgggtggagcaacagtcagtgaggctagtggtgaaaaatta
 cctagtcaggtgtttaatcatctgaagattgcggttattctagtggttggatgaatta
 aaatttcaggctaaagagatgtatgggttaccagccttcccactcttatatgaagtttca
 acaatttctaaaatcagagcaggttttctgtatggacaagcaagtagtgcgaaacaattg
 aaaaagaataatttaccagccctcttattcatggtgataaggataatttgttccaaca
 agtatgggttatgacaactataaagctacagcaggttaagaaagagctttatattgtaaaa
 ggggcaaacatgcgaatcttttgaacagagccagaaaaatatgagaaacgtatctct
 agttttttgaaaaaatatgaaaaa

SEQ ID NO. 8302

STRAIN 090

GCTAGTTTTATTTTTTCCACGTTGCCCAAGTTCC
 AGATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTT
 TATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAATAGAA
 ATGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAA
 GAAAACTCATAAGACAGCTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAG
 AGAATATGAAGGCATATGGTTGGCTGTTCATAAGTTAGGATACAATGTT
 CTATGCTGACATATGTCACATGGTGAAAGTCATGGGCAGTTGATAGG
 CTATGGCTGGAACGACCGCGAGAACATTATCAATGGACAGAAATGATAG
 TTGATAAGAATCCATCAAGCCAAATTACTTTaTTTGGTGTTCATGGGT
 GGAGCAACAGCTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGT
 TAATATCATTTGAAGATTGCGGTTATTCTAGTGTTTGGGATGAATTAATA
 TTCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACCTCTTATATGAA
 GTTTCACAAATTTCTAAAATCAGAGCAGGTTTTCTGTATGGACAAGCAAG
 TAGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATG
 GTGATAAGGATAATTTTGTTCACCAAGTATGGTTTATGACAACTATAAAA
 GCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAGGGGCAAAACATGC
 GAAATCTTTTGAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTT
 TTTTGA AAAAATATGAAAAA

SEQ ID NO. 8303

STRAIN A909

AATCCTTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTTATATGCT
 TATGATAAATCCTTTGATAAGCTATTAAAGCAAAAATAGAAATGACAAA
 CCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGAAAACTC
 ATAAGACAGCTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAGAGAATATG
 AAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTCTTATGCC
 TGACAACTATGCACATGGTGAAAGTCATGGGCAGTTGATAGGCTATGGCT
 GGAACGACCGCGAAGCAATATCAATGGACAGAAATGATAGTTGATAAG
 AATTCTATCAAGCCAAATTACTTTATTGGTGTTCATGGGTGGAGCAAC
 AGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTAATATCA
 TTGAAGATGCGGTTATTCTGGTGTTTGGGATGAATTAATAATTCAGGCT
 AAAGAGATGTATGGTTTACCAGCCTTCCCACCTCTTATATGAAGTTTCAAC
 AATTTCTAAAATCAGAGCAGGTTTTCTGTATGGACAAGCAAGTAGTGTG
 AACAAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATGGTGATAAG
 GATAATTTTGTTCACCAAGATAGGTTTATGACAACTATAAGCTACAGC
 AGGTAAGAAAGAGCTTTATATTGTAAAGGGGCAAAACATGCGAAATCTT
 TTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTTTTTGAAA
 AAATATGAAAAA

SEQ ID NO. 8304

STRAIN H36B

AGTTTTTATTTTTTCCACGTTGCCCAAGTTTCGAGATGATAAATCCTTTAT
 TTCAAATGGTCAACGTAAGCCTGGAAACTCTTTATATGCTTATGATAAAT
 CCTTTGATAAGCTATTAAAGCAAAAATAGAAATGACAAACCAAAATATA
 AAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGAAAACTCATAAGACAGC
 GTTGTGCTTCATGGTTTTGCGAATAGCAAAGAGAATATGAAGGCATATG
 GTTGGCTGTTTCATAAGTTAGGATACAATGTTCTTATGCTGACAACTAT
 GCACATGGTGAAAGTCATGGGCAGTTGATAGGCTATGGCTGGAACGACCG
 CGAGAACATTATCAAAATGGACAGAAATGATAGTTGATAAGAAATTCATCAA
 GCCAAATTACTTTATTGGTGTTCATGGGTGGAGCAACAGTCATGATG
 GCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTAATATCATTGAAGATTG
 CGGTTATTCTGGTGTTTGGGATGAATTAATAATTCAGGCTAAAGAGATGT
 ATGGTTTACCAGCCTTCCCACCTCTTATATGAAGTTTCAACAATTTCTAAA
 ATCAGAGCAGGTTTTCTGTATGGACAAGCAAGTAGTGTGCAACAATTGAA
 AAAGAATAATTTACCAGCCCTCTTTATTTCATGGTGATAAGGATAATTTTG
 TTCCAACAAGTATGGTTTATGACAACTATAAGCTACAGCAGGTAAGAAA
 GAGCTTTATATTGTAAAGGGGCAAAACATGCGAAATCTTTTGAACAGA
 GCCAGAAAAATATGAGAAACGTATCTCTAGTTTTTTGAAAAAATATGAAA
 AA

SEQ ID NO. 8305

STRAIN 18RS21

Table 83: Comparative Sequences relating to SAG0108

GCTAGTTTTATTTTTTCCACGTTGCCCAAGTTCGA
 GATGATAAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTT
 ATATGCTTTATGATAAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
 TGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTCTGCTGTTAAG
 AAAACTCATAGACAGCTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAGA
 GAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTTC
 TTATGCTTGACAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGC
 TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
 TGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTG
 GAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
 AATATCATTGAAGATTGCGGTTATTCTAGTGTGGGATGAATTAATAAT
 TCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAG
 TTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGT
 AGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATGG
 TGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAAAG
 CTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCG
 AAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTT
 TTTGAAAAAATATGAAAAA

SEQ ID NO. 8306

STRAIN M732

GCTAGTTTTATTTTTTCCACGTTGCCCAAGTTCGA
 GATGATAAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTT
 ATATGCTTTATGATAAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
 TGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTCTGCTGCTAAG
 AAAACTCATAGACAGTTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAGA
 GAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTTC
 TTATGCTTGACAACATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGC
 TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
 GGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTCATGGGTG
 GAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
 AATATCATTGAAGATTGTTGTTTATTCTAGTGTGGGATGAATTAATAAT
 TCAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAG
 TTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGT
 AGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCATGG
 TGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAAAG
 CTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCG
 AAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTT
 TTTGAAAAAATATGAAAAA

SEQ ID NO. 8307

STRAIN COH1

GCTAGTTTTATTTTTTCCACGTTGCCCAAGTTC
 GAGATGATAAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCT
 TTATATGCTTTATGATAAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGA
 AATGaCAAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTCTGCTGCTA
 AGAAAACTCATAGACAGTTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAA
 GAGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGT
 TCTTATGCTTGACAACATTGCACATGGTGAAAGTCATGGGCAGTTGATAG
 CTATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATA
 GTGGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTG
 TGGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTG
 TTAATATCATTGAAGATTGTTGTTTATTCTAGTGTGGGATGAATTAATAA
 TTTCAAGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGA
 AGTTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAA
 GTAGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCAT
 GGTGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAA
 AGCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATG
 CGAAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGT
 TTTTGAAAAAATATGAAAAA

SEQ ID NO. 8308

STRAIN M781

GCTAGTTTTATTTTTTCCACGTTGCCCAAGTTCG
 AGATGATAAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTT
 TATATGCTTTATGATAAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAA
 ATGACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTCTGCTGCTAA
 GAAACTCATAGACAGTTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAG
 AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
 CTTATGCTTGACAACATTGCACATGGTGAAAGTCATGGGCAGTTGATAGG
 CTATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAG
 TGGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTCATGGGTG
 GGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
 TAAATATCATTGAAGATTGTTGTTTATTCTAGTGTGGGATGAATTAATAA
 TTTCAAGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGA
 GTTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAA
 GTAGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTCAT
 GGTGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAA
 AGCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATG
 CGAAATCTTTTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGT
 TTTTGAAAAAATATGAAAAA

SEQ ID NO. 8309

Table 83: Comparative Sequences relating to SAG0108

STRAIN CJB110

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCGAG
 ATGATAAATCCCTTTATTTCAAATGGTCAACGTAAGCCTGGAACTCTTTA
 TATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAAT
 GACAAACCAAAATATAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGA
 AAACCTATAAGACAGCTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAGAG
 AATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTcT
 TATGCTGTGACAAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGGCT
 ATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGTT
 GATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTGG
 AGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTA
 ATATCATTGAAGATTGCGGTTATTcTAGTGTTTGGGATgAATTAAAAATTT
 CAGGCTAAAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAGT
 TTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGTA
 gTGTGGAACAATTGAAAAAGAAATAATTACCAGCCCTcTTTATTATGAGT
 GATAAGGATAAATTTTGTTCACAAGATATGGTTTATGACAACATAAAGC
 TACAGCAGGTAAAGAAAGAGCTTTATATTTGTAAGGGGGCAAAACATGCGA
 AATCTTTTGAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTTT
 TTGAAAAAATATGAAAAA

SEQ ID NO. 8310

STRAIN 1169NT

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCGA
 GATGATAAATCCCTTTATTTCAAATGGTCAACGTAAGCCTGGAACTCTTT
 ATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAAA
 TGACAAACCcAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAG
 AAAACCTATAAGACAGCTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAGA
 gAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTc
 TTATACCTGACAAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGG
 TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
 TGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTGG
 GAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
 AATATCATTGAAGATTgCGGTTATTcTAGTGTTTGGGATgAATTAAAAAT
 TCAGGCTAaAGAGATGTATGGTTTaCCAGCCTTCCCACTcTTATATGAAG
 TTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGT
 AGTGTAGAACAAATTGAAAAAGAAATAATTACCAGCCCTCTTTATTATGAG
 TGATAAGGATAAATTTTGTTCACAAGATATGGTTTATGACAACATAAAG
 CTACAGCAGGTAAAGAAAGAGCTTTATATTTGTAAGGGGGCAAAACATGCG
 AATCTTTTGAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTTT
 TTTGAAAAAATATGAAAAA

SEQ ID NO. 8311

STRAIN JM9130013

GCTAGTTTTTATTTTTTCCACGTTGCCCAAGTTCG
 AGATGATAAATCCCTTTATTTCAAATGGTCAACGTAAGCCTGGAACTCTTT
 TATATGCTTATGATAAATCCTTTGATAAGCTATTAAAGCAAAAAATAGAA
 ATGaCAAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCTGCTGTTAA
 GAAAACTCATAAGACAGCTGTTGTCGTTTCATGGTTTTGCGAATAGCAAAG
 AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
 CTATGCTGTGACAAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGG
 CTATGGCTGGAACGACCGCGAGAACATTATCaAATGGACAGAAATGATAG
 TTGATAAGAATCCATCAAGCCAAATTaCTTTATTTGGTGTTCATGGGT
 GGAGCAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGT
 TAATATCATTGAAGATTGCGGTTATTcTAGTGTTTGGGATgAATTAAAAAT
 TTCAAGCTAaAGAGATGTATGGTTTACCAGCCTTCCCACTCTTATATGAAG
 GTTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAG
 TAGTGTGGAACAATTGAAAAAGAAATAATTACCAGCCCTCTTTATTATG
 GTGATAAGGATAAATTTTGTTCACAAGATATGGTTTATGACAACATAAAG
 GCTACAGCAGGTAAAGAAAGAGCTTTATATTTGTAAGGGGGCAAAACATGCG
 GAAATCTTTTGAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTT
 TTTTGAAAAAATATGAAAAA

PRETTY of: /biotmp/msa286608.2{*} February 24, 2003 06:26 ..

	1				50
msa286608.2{662_COH1}	-----	-----	-----	-----	-----
msa286608.2{662_M732}	-----	-----	-----	-----	-----
msa286608.2{662_M781}	-----	-----	-----	-----	-----
msa286608.2{662_A909}	-----	-----	-----	-----	-----
msa286608.2{662_H36B}	-----	-----	-----	-----	-----
msa286608.2{662_090}	-----	-----	-----	-----	-----
msa286608.2{662_CJB110}	-----	-----	-----	-----	-----
msa286608.2{662_18RS21}	-----	-----	-----	-----	-----
msa286608.2{662_2603}	atgaaaaaga	ttcgattatc	aaagtttatt	aaaatgattg	ttgtattttt
msa286608.2{662_JM9130013}	-----	-----	-----	-----	-----
msa286608.2{662_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****

	51				100
msa286608.2{662_COH1}	-----	-----g	ctagttttta	ttttttccac	gttgcccaag
msa286608.2{662_M732}	-----	-----g	ctagttttta	ttttttccac	gttgcccaag
msa286608.2{662_M781}	-----	-----g	ctagttttta	ttttttccac	gttgcccaag

Table 83: Comparative Sequences relating to SAG0108

msa286608.2{662_A909}	-----	-----	-----	-----	-----
msa286608.2{662_H36B}	-----	-----	-----	-----	-----
msa286608.2{662_090}	-----	-----	-----	-----	-----
msa286608.2{662_CJB110}	-----	-----	-----	-----	-----
msa286608.2{662_18RS21}	-----	-----	-----	-----	-----
msa286608.2{662_2603}	gtttttaatt	agtgttagcag	ctagttttta	ttttttccac	gttgcccaag
msa286608.2{662_JM9130013}	-----	-----	-----	-----	-----
msa286608.2{662_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	-----	-----	-----
msa286608.2{662_COH1}	101	151	201	250	300
msa286608.2{662_M732}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCACGTAA	GCCTGGAAAC
msa286608.2{662_M781}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCACGTAA	GCCTGGAAAC
msa286608.2{662_A909}	-----	-----	-----	-----	-----
msa286608.2{662_H36B}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCACGTAA	GCCTGGAAAC
msa286608.2{662_090}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCACGTAA	GCCTGGAAAC
msa286608.2{662_CJB110}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCACGTAA	GCCTGGAAAC
msa286608.2{662_18RS21}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCACGTAA	GCCTGGAAAC
msa286608.2{662_2603}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCACGTAA	GCCTGGAAAC
msa286608.2{662_JM9130013}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCACGTAA	GCCTGGAAAC
msa286608.2{662_1169NT}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCACGTAA	GCCTGGAAAC
Consensus	-----	*****	*****	*****	*****
msa286608.2{662_COH1}	151	201	250	300	350
msa286608.2{662_M732}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_M781}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_A909}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_H36B}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_090}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_CJB110}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_18RS21}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_2603}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_JM9130013}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
msa286608.2{662_1169NT}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	201	250	300	350	400
msa286608.2{662_M732}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_M781}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_A909}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_H36B}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_090}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_CJB110}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_18RS21}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_2603}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_JM9130013}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
msa286608.2{662_1169NT}	AGAAATGACA	AACCAAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCTGCTG
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	251	300	350	400	450
msa286608.2{662_M732}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_M781}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_A909}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_H36B}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_090}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_CJB110}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_18RS21}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_2603}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_JM9130013}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
msa286608.2{662_1169NT}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGCG	TTCATGGTTT	TGCGAATAGC
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	301	350	400	450	500
msa286608.2{662_M732}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_M781}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_A909}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_H36B}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_090}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_CJB110}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_18RS21}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_2603}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_JM9130013}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
msa286608.2{662_1169NT}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	351	400	450	500	550
msa286608.2{662_M732}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_M732}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA

Table 83: Comparative Sequences relating to SAG0108

msa286608.2{662_M781}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_A909}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_H36B}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_090}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_CJB110}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_18RS21}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_2603}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_JM9130013}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_1169NT}	TGTTCTTATa	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
Consensus	*****-*****	*****-*	*****	*****	*****
msa286608.2{662_COH1}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_M732}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_M781}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_A909}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_H36B}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_090}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_CJB110}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_18RS21}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_2603}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_JM9130013}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_1169NT}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	ATAGTgGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_M732}	ATAGTgGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_M781}	ATAGTgGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_A909}	ATAGTtGATA	AGAATtCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_H36B}	ATAGTtGATA	AGAATtCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_090}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_CJB110}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_18RS21}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_2603}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_JM9130013}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_1169NT}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_M732}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_M781}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_A909}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_H36B}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_090}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_CJB110}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_18RS21}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_2603}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_JM9130013}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_1169NT}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_M732}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_M781}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_A909}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTgGTGTTTg	GGATGAATTA
msa286608.2{662_H36B}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTgGTGTTTg	GGATGAATTA
msa286608.2{662_090}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_CJB110}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_18RS21}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_2603}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_JM9130013}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_1169NT}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
Consensus	*****	*****	**..*****	**..*****	*****
msa286608.2{662_COH1}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTTATA
msa286608.2{662_M732}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTTATA
msa286608.2{662_M781}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTTATA
msa286608.2{662_A909}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTTATA
msa286608.2{662_H36B}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTTATA
msa286608.2{662_090}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTTATA
msa286608.2{662_CJB110}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTTATA
msa286608.2{662_18RS21}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTTATA
msa286608.2{662_2603}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTTATA
msa286608.2{662_JM9130013}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTTATA
msa286608.2{662_1169NT}	AAATTTcAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACtCTTATA
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG

Table 83: Comparative Sequences relating to SAG0108

msa286608.2{662_M732}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_M781}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_A909}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_H36B}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_090}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_CJB110}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_18RS21}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_2603}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_JM9130013}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
msa286608.2{662_1169NT}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTCG	TATGGACAAG
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTACCAGC	CCTCTTTATT
msa286608.2{662_M732}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTACCAGC	CCTCTTTATT
msa286608.2{662_M781}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTACCAGC	CCTCTTTATT
msa286608.2{662_A909}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTACCAGC	CCTCTTTATT
msa286608.2{662_H36B}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTACCAGC	CCTCTTTATT
msa286608.2{662_090}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTACCAGC	CCTCTTTATT
msa286608.2{662_CJB110}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTACCAGC	CCTCTTTATT
msa286608.2{662_18RS21}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTACCAGC	CCTCTTTATT
msa286608.2{662_2603}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTACCAGC	CCTCTTTATT
msa286608.2{662_JM9130013}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTACCAGC	CCTCTTTATT
msa286608.2{662_1169NT}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTACCAGC	CCTCTTTATT
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_M732}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_M781}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_A909}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_H36B}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_090}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_CJB110}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_18RS21}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_2603}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_JM9130013}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_1169NT}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_M732}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_M781}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_A909}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_H36B}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_090}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_CJB110}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_18RS21}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_2603}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_JM9130013}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_1169NT}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_M732}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_M781}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_A909}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_H36B}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_090}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_CJB110}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_18RS21}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_2603}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_JM9130013}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_1169NT}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
Consensus	*****	*****	*****	*****	*****
msa286608.2{662_COH1}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_M732}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_M781}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_A909}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_H36B}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_090}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_CJB110}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_18RS21}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_2603}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_JM9130013}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_1169NT}	AGTTTTTTGA	AAAAATATGA	AAAA		
Consensus	*****	*****	*****		

Table 83: Comparative Sequences relating to SAG0108

STRAIN 2603 frame: 1

MKKIRLSKFIKMIIVILFLISVAASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFD
KLLKQKIEMTNQNIKQVAVYVPAVKKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLM
PDNIAHGESHGQLIGYWNDRNI IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKL
PSQVVNI IEDCGYSSVWDELKFKQAKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQL
KKNLPALEFIHGDKNFVPTSMVYDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8313

STRAIN 090 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYWNDRNI
IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8314

STRAIN A909 frame: 3

SFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPAKKTHKTAVVHGF
NSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYWNDRNI IKWTEMIVDKNSS
QITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSGVWDELKFKQAKEMYGLPAFPLLYE
VSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKNFVPTSMVYDNYKATAGKKELYI
VKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8315

STRAIN H36B frame: 1

SFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
KTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYWNDRNI
IKWTEMIVDKNSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSGVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8316

STRAIN 18RS21 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
VKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYWNDRNI
IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8317

STRAIN M732 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYWNDRNI
IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8318

STRAIN COH1 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYWNDRNI
IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8319

STRAIN M781 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYWNDRNI
IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8320

STRAIN CJB110 frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYWNDRNI
IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8321

STRAIN 1169NT frame: 1

ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
AKKTHKTAVVHGFANSKENMKAYGWLPHKLGYNVLI PDNIAHGESHGQLIGYWNDRNI
IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVVNI IEDCGYSSVWDELKFKQ
AKEMYGLPAFPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKNFVPTSMV
YDNYKATAGKKELYIVKGAKHAKSFETEPEKEYEKRISSFLKKYEK

SEQ ID NO. 8322

Table 83: Comparative Sequences relating to SAG0108

STRAIN JM9130013 frame: 1

ASFYFFHVAQVRDDKSF ISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAVYVPA
 VKKTHKTAVVVHGFANSKENMKAYGWL FHLGYNVLPDNIHAGESHGQLIGYGNDRN
 I IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLP SQVVNI IEDCGYSSVWDELKFO
 AKEMYGLPAFPLLYEVSTISKIRAGFSYQASSVEQLKKNLPALEI HGDKNFVPTSMV
 YDNYKATAGKELYIVGAKHAKSFETEPEKYEKRISFLKKYK

PRETTY of: /biotmp/msa286876.2{*} February 24, 2003 06:46 ..

	1				50
msa286876.2{662_A909}	-----	-----	-----	-----SF	ISNGQRKPGN
msa286876.2{662_H36B}	-----	-----	---SFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_COH1}	-----	-----	---ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_M732}	-----	-----	---ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_M781}	-----	-----	---ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_18RS21}	-----	-----	---ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_2603}	mkkirlskfi	kmivvilfli	svaASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_JM9130013}	-----	-----	---ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_090}	-----	-----	---ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_CJB110}	-----	-----	---ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_1169NT}	-----	-----	---ASFYFFH	VAQVRDDKSF	ISNGQRKPGN
Consensus	*****	*****	*****	*****	*****
	51				100
msa286876.2{662_A909}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_H36B}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_COH1}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_M732}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_M781}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_18RS21}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_2603}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_JM9130013}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_090}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_CJB110}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAVY	VPAaKKTHTK	avVVHGFANS
msa286876.2{662_1169NT}	SLYAYDKSFD	KLLKQKIEMT	NQNIKQVAVY	VPAaKKTHTK	avVVHGFANS
Consensus	*****	*****	*****	*****	*****
	101				150
msa286876.2{662_A909}	KENMKAYGWL	FHLGYNVLM	PDNIHAGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_H36B}	KENMKAYGWL	FHLGYNVLM	PDNIHAGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_COH1}	KENMKAYGWL	FHLGYNVLM	PDNIHAGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_M732}	KENMKAYGWL	FHLGYNVLM	PDNIHAGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_M781}	KENMKAYGWL	FHLGYNVLM	PDNIHAGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_18RS21}	KENMKAYGWL	FHLGYNVLM	PDNIHAGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_2603}	KENMKAYGWL	FHLGYNVLM	PDNIHAGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_JM9130013}	KENMKAYGWL	FHLGYNVLM	PDNIHAGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_090}	KENMKAYGWL	FHLGYNVLM	PDNIHAGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_CJB110}	KENMKAYGWL	FHLGYNVLM	PDNIHAGESH	GQLIGYGWND	RENI IKWTEM
msa286876.2{662_1169NT}	KENMKAYGWL	FHLGYNVLM	PDNIHAGESH	GQLIGYGWND	RENI IKWTEM
Consensus	*****	*****	*****	*****	*****
	151				200
msa286876.2{662_A909}	IVDKNsSSQI	TLFGVSMGGA	TVMASGEKL	PSQVVNIIED	CGYSgVWDEL
msa286876.2{662_H36B}	IVDKNsSSQI	TLFGVSMGGA	TVMASGEKL	PSQVVNIIED	CGYSgVWDEL
msa286876.2{662_COH1}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVVNIIED	CGYSsVWDEL
msa286876.2{662_M732}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVVNIIED	CGYSsVWDEL
msa286876.2{662_M781}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVVNIIED	CGYSsVWDEL
msa286876.2{662_18RS21}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVVNIIED	CGYSsVWDEL
msa286876.2{662_2603}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVVNIIED	CGYSsVWDEL
msa286876.2{662_JM9130013}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVVNIIED	CGYSsVWDEL
msa286876.2{662_090}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVVNIIED	CGYSsVWDEL
msa286876.2{662_CJB110}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVVNIIED	CGYSsVWDEL
msa286876.2{662_1169NT}	IVDKNpSSQI	TLFGVSMGGA	TVMASGEKL	PSQVVNIIED	CGYSsVWDEL
Consensus	*****	*****	*****	*****	*****
	201				250
msa286876.2{662_A909}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEI
msa286876.2{662_H36B}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEI
msa286876.2{662_COH1}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEI
msa286876.2{662_M732}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEI
msa286876.2{662_M781}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEI
msa286876.2{662_18RS21}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEI
msa286876.2{662_2603}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEI
msa286876.2{662_JM9130013}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEI
msa286876.2{662_090}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEI
msa286876.2{662_CJB110}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEI
msa286876.2{662_1169NT}	KFQAKEMYGL	PAFPLLYEVS	TISKIRAGFS	YGQASSVEQL	KKNLPALEI
Consensus	*****	*****	*****	*****	*****
	251				300
msa286876.2{662_A909}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_H36B}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_COH1}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS

Table 83: Comparative Sequences relating to SAG0108

msa286876.2{662_M732}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_M781}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_18RS21}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_2603}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_JM9130013}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_090}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_CJB110}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_1169NT}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
Consensus	*****	*****	*****	*****	*****
301					
msa286876.2{662_A909}	SFLKKYEK				
msa286876.2{662_H36B}	SFLKKYEK				
msa286876.2{662_COH1}	SFLKKYEK				
msa286876.2{662_M732}	SFLKKYEK				
msa286876.2{662_M781}	SFLKKYEK				
msa286876.2{662_18RS21}	SFLKKYEK				
msa286876.2{662_2603}	SFLKKYEK				
msa286876.2{662_JM9130013}	SFLKKYEK				
msa286876.2{662_090}	SFLKKYEK				
msa286876.2{662_CJB110}	SFLKKYEK				
msa286876.2{662_1169NT}	SFLKKYEK				
Consensus	*****				

Table 84: Comparative Sequences relating to SAG0267

SEQ ID NO. 8401

STRAIN 2603

ATGATGAAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCAGTGGCTGTACTAAAC
 AATATGGAATGTTTAGCGACTGTCACTATCAATATCAAAAAGAAATCATAGCATTAAATTTG
 ATGCCAGCCATTGATTTTAAATGCAATCAATTGATTAGAACCTCAAGATTGGACCGT
 ATCGTAGTAGCAGAGGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGTACAGCA
 AAAATGCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGCTTTA
 ACAAATGGATTTTCAGAAAATGATTTATTTGGTACCCTTATAGATGCACGACGTAATAAT
 GTTTATGTTGGTTTCTATCAAAATGGTGATACTGTTAAACCAGACTGTACACTTCTCTT
 GAAGAAGTCTTACAAGAGGTGGGGAATAAAGCCAATGTTTATTGTCGGAGAGGTTGCA
 GCATTTTGTGATCAGATTAAAGAAAGCCTTACCACATGCTAAAATTACAGAAACCTTTACCT
 TGTGCAGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATGCGTTT
 GTTCCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTAAAAAACCACTGTGAA
 ACGAATACAGAAGATATATTAAAGAGAGTT

SEQ ID NO. 8402

STRAIN 090

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCAGTGGCTGTACT
 AAACAATATGGAATGTTTAGCGACTGTCACTATCAATATCAAAAAGAAATC
 ATAGCATTAAATTTGATGCCAGCCATTGATTTTAAATGCAATCAATTGAT
 TTAGAACCCTCAAGATTGGACCGTATCGTAGTGGCAGAGGGTCCAGGATC
 TTATACGGGCTTACGTGTAGCTGTTGTACAGCAAAAATGCTAGCTTATA
 CGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGCTTTAAACAAT
 GGATTTTCAGAAAATGATTTGTTGGTACCCTTATAGATGCACGACGTAA
 CAATGTTTATGTTGGTTTCTATCAAAATGGTGATACTGTTAAACCAGACT
 GTACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGAATAAAGCCAAT
 GTTCATTTTGTGCGAGAGGTTGCAGCATTTTGTGATCAGATTAAAGAAAGC
 CTTACCACATGCTAAAATTACAGAAACCTTTACCTTGTGCAGTGGCAATTG
 GCGCAAGAGGACAAAAATGGAAGCGTTAATGTAGATGCGTTTGTTCAC
 CGATACTTAAAACGAGTTGAAGCTGAGGAAAATTGGTTAAAAAACCACTG
 TGAACGAAT

SEQ ID NO. 8403

STRAIN A909

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCAG
 TGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATATC
 AAAAAAGAAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTAAATGCA
 ATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAGCAGAGG
 GTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGTCTACAGCAAAAATG
 CTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGC
 TTTAAACAAATGGATTTTCAGAAAATGATTTATTTGGTACCCTTATAGATG
 CACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGTT
 AAACCAGACTGTACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 TAAAGCCAATGTTTCAATTTGTGCGAGAGGTTGCAGCATTTGTTGACCAGA
 TTAAGAAAGTTTACCACATGCTAAAATTACAGAACTTTACCTTGTGCA
 GCGGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATGC
 GTTTGTTCCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTAA
 GAAACCACTGTGAACGAAT

SEQ ID NO. 8404

STRAIN H36B

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAAGAAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTAAATGC
 AATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAGCAGAG
 GGTCAGGATCTTATACGGGCTTACGTGTAGCTGTTGTCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAAACAAATGGATTTTCAGAAAATGATTTATTTGGTACCCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGT
 TAAACCAAGCTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTCAATTTGTGCGAGAGGTTGCAGCATTTGTTGACCAG
 ATTAAGAAAGTTTACCACATGCTAAAATTACAGAACTTTACCTTGTGCA
 AGTGGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATG
 CGTTTGTTCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTA
 AGAAACCACTGTGAACGAATACAGAAGATATATTAAAGAGAGTT

SEQ ID NO. 8405

STRAIN 18RS21

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAAGAAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTAAATGC
 AATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAGCAGAG
 GGTCAGGATCTTATACGGGCTTACGTGTAGCTGTTGTCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAAACAAATGGATTTTCAGAAAATGATTTATTTGGTACCCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGT
 TAAACCAAGCTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTCAATTTGTGCGAGAGGTTGCAGCATTTTGTGACCAG
 ATTAAGAAAGTTTACCACATGCTAAAATTACAGAACTTTACCTTGTGCA
 AGTGGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATG
 CGTTTGTTCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTA
 AGAAACCACTGTGAACGAATACAGAAGATATATTAAAGAGAGTT

Table 84: Comparative Sequences relating to SAG0267

SEQ ID NO. 8406

STRAIN M732

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGC
 AATCAATTGATTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
 GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAAACAAATGGATTTTCAGAAAATGATTTATTGGTACCACCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGACTGT
 TAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTTTTTGATCAG
 ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
 AGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGAnn
 CGTTTGTTCACGATACCTTAAACGTTGTAAGCTGAGGAAAATTGGTTA
 AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO. 8407

STRAIN COH1

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCAC
 TATCAGTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATC
 AATATCAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTT
 AATGCAATCAATTGATTAGAACCTCAAGATTTGGACCGTATCGTAGTAG
 CAGAGGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCA
 AAAATGCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCT
 GTACGCTTTAACAATGGATTTTCAGAAAATGATTTATTGGTACCACCTTA
 TAGATGCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGAT
 ACTGTTAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGT
 GGGGAATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTTTTTG
 ATCAGATTAAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCT
 TGTGCAGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGT
 AGATGCGTTTGTTCACGATACCTTAAACGTTGTAAGCTGAGGAAAATT
 GGTAAAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO. 8408

STRAIN M781

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTA
 TCAGTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAA
 TATCAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAA
 TGCAATCAATTGATTAGAACCTCAAGATTTGGACCGTATCGTAGTATCA
 GAGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAA
 AATGCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGT
 ACGCTTTAACAATGGATTTTCAGAAAATGATTTATTGGTACCACCTTATA
 GATGCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGATA
 TGTTAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGG
 GGAATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTTTTTGAT
 CAGATTAAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTG
 TGCAGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAG
 ATGCGTTTGTTCACGATACCTTAAACGTTGTAAGCTGAGGAAAATTGGT
 TAAAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO. 8409

STRAIN CJB110

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGC
 AATCAATTGATTAGAACCTCAAGATTTGGACCGTATCGTAGTGGCAGAG
 GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAAACAATGGATTTTCAGAAAATGATTTGTTGGTACCACCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGACTGT
 TAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTTTTTgATCAG
 ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
 AGTGGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATG
 CGTTTGTTCACGATACCTTAAACGAGTTGAAGCTGAGGAAAATTGGTTA
 AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO. 8410

STRAIN I169NT

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGC
 AATCAATTGATTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
 GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTTAAACAATGGATTTTCAGAAAATGATTTATTGGTACCACCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGTGACTGT
 TAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTCATTTTGTGCGAGAGGTTGCAGCATTTTTTgATCAG
 ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
 AGTGGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATG
 CGTTTGTTCACGATACCTTAAACGAGTTGAAGCTGAGGAAAATTGGTTA
 AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

Table 84: Comparative Sequences relating to SAG0267

AGTGGCAATTGGGCGCAAAGGACAAAAATGGAAGCGTTAATGTAGATG
CGTTTGTTCACGATACCTTAAACGTGTTGAAGCTGAGGAAATTTGGTTA
AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

SEQ ID NO.: 8411

STRAIN JM9130013

AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCA
GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
CAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTAATGC
AATCAATTGATTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
gCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
CTTTAACAATATGATTTTCAGAAAATGATTTATTGGTACCCTTATAGAT
GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGT
TAAACCAAGCTGTCACTTCTCTTGAAGAAGCTTACAAGAGGTGGGGA
ATAAAGCCAATGTTTCAATTTTGTGCGAGAGGTTGCAGCATTGTTGACCAG
ATTAAGAAAGTTTACCACATGCTAAAATTACAGAAACCTTACCTTGTGC
AGTGGCAATTGGGCGCAAAGGACAAAAATGGAAGCGTTAATGTAGATG
CGTTTGTTCACGATACCTTAAACGTGTTGAAGCTGAGGAAATTTGGTTA
AGAAACCACTGTGAAACGAATACAGAAGAATATATTAAAGAGAGTT

PRETTY of: /biotmp/msa521675.2{*} March 10, 2003 08:34 ..

	1		50
msa521675.2{69_A909}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_H36B}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_JM9130013}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_1169NT}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_090}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_CJB110}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_18RS21}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_2603}	atgatgAAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_COH1}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_M732}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_M781}	-----AAAG	TTTTAGCCTT	TGATACTTCA AGCAAAGCAC TATCAGTGGC
Consensus	*****	*****	*****

	51		100
msa521675.2{69_A909}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_H36B}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_JM9130013}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_1169NT}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_090}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_CJB110}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_18RS21}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_2603}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_COH1}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_M732}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
msa521675.2{69_M781}	TGTACTAAAC	AATATGGAAT	GTTTAGCGAC TGTCACATC AATATCAAAA
Consensus	*****	*****	*****

	101		150
msa521675.2{69_A909}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_H36B}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_JM9130013}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_1169NT}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_090}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_CJB110}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_18RS21}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_2603}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_COH1}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_M732}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_M781}	AGAATCATAG	CATTAATTG	ATGCCAGCCA TTGATTTTTT AATGCAATCA
Consensus	*****	*****	*****

	151		200
msa521675.2{69_A909}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_H36B}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_JM9130013}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_1169NT}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_090}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_CJB110}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_18RS21}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_2603}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_COH1}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_M732}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
msa521675.2{69_M781}	ATTGATTAG	AACCTCAAGA	TTTGGACCGT ATCGTAGTg CAGAGGGTCC
Consensus	*****	*****	*****

	201		250
msa521675.2{69_A909}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT TGCTACAGCA AAAATGCTAG
msa521675.2{69_H36B}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT TGCTACAGCA AAAATGCTAG

Table 84: Comparative Sequences relating to SAG0267

msa521675.2{69_JM9130013}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_1169NT}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_090}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_CJB110}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_18RS21}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_2603}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_COH1}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_M732}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
msa521675.2{69_M781}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAAATGCTAG
Consensus	*****	*****	*****	*****	*****
251					
msa521675.2{69_A909}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_H36B}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_JM9130013}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_1169NT}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_090}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_CJB110}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_18RS21}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_2603}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_COH1}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_M732}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_M781}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
Consensus	*****	*****	*****	*****	*****
301					
msa521675.2{69_A909}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_H36B}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_JM9130013}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_1169NT}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_090}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_CJB110}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_18RS21}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_2603}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_COH1}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_M732}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_M781}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
Consensus	*****	*****	*****-***	*****	*****
351					
msa521675.2{69_A909}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGaGAT	ACTGTTAAAC
msa521675.2{69_H36B}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGaGAT	ACTGTTAAAC
msa521675.2{69_JM9130013}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGaGAT	ACTGTTAAAC
msa521675.2{69_1169NT}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_090}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_CJB110}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_18RS21}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_2603}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_COH1}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_M732}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_M781}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
Consensus	*****-***	*****	*****	*****-***	*****
401					
msa521675.2{69_A909}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_H36B}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_JM9130013}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_1169NT}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_090}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_CJB110}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_18RS21}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_2603}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_COH1}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_M732}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_M781}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
Consensus	*****	*****	*****	*****	*****
451					
msa521675.2{69_A909}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_H36B}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_JM9130013}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_1169NT}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_090}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_CJB110}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_18RS21}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_2603}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_COH1}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_M732}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
msa521675.2{69_M781}	GCCAAATGTTT	ATTTTGTGCG	AGAGGTTGCA	GCATTtGTTG	AcCAGATTAA
Consensus	*****	*****	*****	*****-***	*-*****
501					
msa521675.2{69_A909}	GAAAGtTTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
550					

Table 84: Comparative Sequences relating to SAG0267

msa521675.2{69_H36B}	GAAAGcttTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_JM9130013}	GAAAGcttTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_1169NT}	GAAAGcttTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_090}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_CJB110}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_18RS21}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_2603}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_COH1}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_M732}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_M781}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
Consensus	*****-***	*****	*****	*****	*****
msa521675.2{69_A909}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_H36B}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_JM9130013}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_1169NT}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_090}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_CJB110}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_18RS21}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_2603}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_COH1}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_M732}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_M781}	CAATTGGGCG	CAAAGGACAA	AAAATGaAAA	CGGTTAATGT	AGAtgCGTTT
Consensus	*****	*****	*****-***	*****	*****
msa521675.2{69_A909}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAgAAA
msa521675.2{69_H36B}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAgAAA
msa521675.2{69_JM9130013}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAgAAA
msa521675.2{69_1169NT}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_090}	GTTCACGAT	ACTTAAAACG	aGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_CJB110}	GTTCACGAT	ACTTAAAACG	aGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_18RS21}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_2603}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_COH1}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_M732}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_M781}	GTTCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
Consensus	*****	*****	-*****	*****	*****-***
msa521675.2{69_A909}	CCACTGTGAA	ACGAAT----	-----	-----	690
msa521675.2{69_H36B}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_JM9130013}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_1169NT}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_090}	CCACTGTGAA	ACGAAT----	-----	-----	
msa521675.2{69_CJB110}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_18RS21}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_2603}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_COH1}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_M732}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_M781}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
Consensus	*****	*****	*****	*****	

SEQ ID NO. 8412

STRAIN 2603 frame: 1

MMKVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDR
 IVVAGPGSYTGLRVAVATAKMLAYTLKIDLGVSSLYALTNGFSENLLVPLIDARRNN
 VYVGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 CAVAIGRKGQKMKSVNVDAFVPRYLKRVEAENWLNHCETNTTEEYIKRV

SEQ ID NO. 8413

STRAIN 090 frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAGPGSYTGLRVAVATAKMLAYTLKIDLGVSSLYALTNGFSENLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEAENWLNHCETN

SEQ ID NO. 8414

STRAIN A909 frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAGPGSYTGLRVAVATAKMLAYTLKIDLGVSSLYALTNGFSENLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEAENWLNHCETN

SEQ ID NO. 8415

STRAIN H36B frame: 1

KVLAFDTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAGPGSYTGLRVAVATAKMLAYTLKIDLGVSSLYALTNGFSENLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDAFVPRYLKRVEAENWLNHCETNTTEEYIKRV

SEQ ID NO. 8416

Table 84: Comparative Sequences relating to SAG0267

STRAIN 18RS21 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGIFYQNGDTVKPDCHTSLSEEVLEQVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKSVNVDAFVPRYLKRVEABENWLKNHCETNTEEYIKRV

SEQ ID NO. 8417

STRAIN M732 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGIFYQNGDTVKPDCHTSLSEEVLEQVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKSVNVXXFVPRYLKRVEABENWLKNHCETNTEEYIKRV

SEQ ID NO. 8418

STRAIN COH1 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGIFYQNGDTVKPDCHTSLSEEVLEQVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKSVNVDAFVPRYLKRVEABENWLKNHCETNTEEYIKRV

SEQ ID NO. 8419

STRAIN M781 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VSEGPSTYGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGIFYQNGDTVKPDCHTSLSEEVLEQVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKSVNVDAFVPRYLKRVEABENWLKNHCETNTEEYIKRV

SEQ ID NO. 8420

STRAIN CJB110 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGIFYQNGDTVKPDCHTSLSEEVLEQVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKSVNVDAFVPRYLKRVEABENWLKNHCETNTEEYIKRV

SEQ ID NO. 8421

STRAIN 1169NT frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGIFYQNGDTVKPDCHTSLSEEVLEQVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKSVNVDAFVPRYLKRVEABENWLKNHCETNTEEYIKRV

SEQ ID NO. 8422

STRAIN JM9130013 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGIFYQNGDTVKPDCHTSLSEEVLEQVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKGQMKSVNVDAFVPRYLKRVEABENWLKNHCETNTEEYIKRV

PRETTY of: /biotmp/msa521982.2{*} March 10, 2003 08:40 ..

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1                                     50
msa521982.2{69_A909} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_H36B} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_JM9130013} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_090} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_CJB110} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_18RS21} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_2603} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_COH1} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_M781} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_1169NT} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_M732} --KVLAFTDS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
Consensus *****
51                                     100
msa521982.2{69_A909} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_H36B} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_JM9130013} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_090} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_CJB110} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_18RS21} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_2603} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_COH1} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_M781} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_1169NT} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_M732} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
Consensus *****
101                                     150
msa521982.2{69_A909} TNGFSENDLL VPLIDARRNN VYVGIFYQNGD TVKPDCHTSL EEVLQEVGNK
msa521982.2{69_H36B} TNGFSENDLL VPLIDARRNN VYVGIFYQNGD TVKPDCHTSL EEVLQEVGNK

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Table 84: Comparative Sequences relating to SAG0267

msa521982.2{69_JM9130013}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_090}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_CJB110}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_18RS21}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_2603}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_COH1}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_M781}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_1169NT}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_M732}	TNGFSENDLL	VPLIDARRNN	VYVGfYQNGD	TVKPDCHTSL	EEVLQEVGNK
Consensus	*****	*****	*****	*****	*****
151					
msa521982.2{69_A909}	ANVHFVGEVA	AFvDQIKKvL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_H36B}	ANVHFVGEVA	AFvDQIKKvL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_JM9130013}	ANVHFVGEVA	AFvDQIKKvL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_090}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMeSVNVdaF
msa521982.2{69_CJB110}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMeSVNVdaF
msa521982.2{69_18RS21}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_2603}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_COH1}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_M781}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_1169NT}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMeSVNVdaF
msa521982.2{69_M732}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVxxF
Consensus	*****	**_*****_*	*****	*****	**_*****_*
201					
msa521982.2{69_A909}	VPRYLKRVEA	EENWLrNHCE	TN-----	230	
msa521982.2{69_H36B}	VPRYLKRVEA	EENWLrNHCE	TNTEEYIKRV		
msa521982.2{69_JM9130013}	VPRYLKRVEA	EENWLrNHCE	TNTEEYIKRV		
msa521982.2{69_090}	VPRYLKRVEA	EENWLkNHCE	TN-----		
msa521982.2{69_CJB110}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_18RS21}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_2603}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_COH1}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_M781}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_1169NT}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
msa521982.2{69_M732}	VPRYLKRVEA	EENWLkNHCE	TNTEEYIKRV		
Consensus	*****	*****	*****		

Table 85: Comparative Sequences relating to SAG1361

SEQ ID NO. 8501

STRAIN 2603

atgagtaaacgcacaaaatttaggaattagtaaaaaaggagcaattatatcagggtctctca
 gtggcactaatgttagtaaataggtgggtttttatgggtacaatctcaacctaatagagt
 gcagtaaaaactaactacaaagtttttatgttagagaaggaggtgttcgtcctcaact
 cttttgcagggaaaagctaaaggctaatcaagaacagtatgtgtattttgatgctaataaa
 ggtaatcgagcaactgtcacagttaaagtgggtgataaaatcacagctgggtcagcagtta
 gttcaabatgatacaacaactgcacaagcagcctacgacactgctaatacgtcaattaaat
 aaagttagcgcgtcagattataatctaagacacaggaagtctccagctatggaatca
 agtgatcaatctcttcatcatcacaaaggacaagggactcaatcgactagtggtgagcag
 aatcgctctacagcaaaattatcaaagtcaagctaagtctcatacaaccaacaactcaa
 gatgttgatgatgcttatgcagatgcacagcgagaaagtaataaagcacaacaaagcattg
 aatgatactgttattacaagtgcgtatcagggacagttgtgaagttaatagtgatatt
 gatccagcttcaaaaactagtcaggtactgttccatgtgacaaactgaaggtaaaactcaa
 gtacaaggaaacgatgagtgagtgatgtttggctaatgttaaaaaagaccaggctgttaaa
 ataaaatctaaggtctatcctgacaaggaatgggaaggtaaaaatttcatatctcaaat
 tatccagaagcagaagcaacaacaatgactctaataacgggtctagtgtgtgtaaatat
 aaatataaagtagatattactagccctctcgatgcattaaaacaaggttttaccgtatca
 gttgaagtagtttaatggagataagcaccttatgtccctacaagtctgtgataaaacaaa
 gataataaacactttgttgggtatacaatgattctaatcgtaaaatttccaaagttgaa
 gtcaaaattggtaagctgtagtgaagacacaagaattttatcaggttgaagcagga
 caaatcggtggttactaatccaagtaaaccttcaaggatgggcaaaaaattgataatatt
 gaatcaatcgatcttaactctaataagaatcagaggtgaaa

SEQ ID NO. 8502

STRAIN 090

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAACTA
 CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
 AAGGTAATCGAGCAACTGTCAAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCTACG
 ACACGTCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAACAGGAAGTCTTCCAGCTATGGAATTAAGTGATCAATCTTCTTC
 ATCATACAAGGACAAGGACTCAATCGACTAGTGGTGGCAGCAATCGTC
 TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAAACTT
 CAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAAGTAAATAAAGC
 ACAAAAAGCATTTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTCAAGTA
 CTTGTCCTATGACCACTGAAGGTAAGTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTTGGCTAATGTTAAAAAGACCAAGGCTGTTAAATAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAATTTTATATATCTCA
 AATTATCCAGAAGCAGAAGCAAAACAATGACTCTAATAACGGCTCTAG
 TGCTGTAATTTATAAATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAAACAAGGTTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATGTCTCCTACAAGTTCTGTGATAAAACAAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAGCA
 GGACAATCGTGGTTACTAATCCAAGTAAACCTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATCGATCTTAACCTAATAAGAAATCAGAGG

SEQ ID NO. 8503

STRAIN A909

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAA
 CTACAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTT
 TGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCT
 AATAAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCAC
 AGCTGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCT
 ACGACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAAT
 CTAAAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTC
 ATCATCTACAAGGACAAGGGCTCAATCGACTAGTGGTGGCAGCAATC
 GTCTACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAA
 CTTCAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAAGTAAATAA
 AGCACAAAAGCATTTGAATGATACTGTTATTACAAGTGACGTATCAGGGA
 CAGTTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAGTCAAGTCA
 GTACTTGTCCATGTAGCAACTGAGGGTAACTCCAAGTACAAGGAACGAT
 GAGTGATATGATTTGGCTAATGTTAAAAAGACCAAGTCTGTTAAATAA
 AATCTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAATTTTATATATC
 TCAAATTATCCAGAAGCAGAAGCAAAACAATGACTCTAATAACGGCTC
 TAGTGCTGTAATTTATAAATAAAGTAGATATTACTAGCCCTCTCGATG
 CATTAAAAACAAGGTTTTACTGTATCAGTTGAAGTAGTTAATGGAGATAAG
 CACCTTATGTTCTTACAAGTTCTGTGACAAAACAAAGATAATAAACACTT
 TGTTTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCA
 AAATTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAG
 GCAGGACAAATCGTGGTTACTAATCCAAGCAAACTTCAAGGATGGGCA
 AAAAATTGATAATATTGAATCAATAGATCTTAAGTCTAATAAGAAATCAG
 AGGTGAAA

SEQ ID NO. 8504

STRAIN H36B

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAATTA
 CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
 AAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAATCACAGC

Table 85: Comparative Sequences relating to SAG1361

TGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCTACG
 ACACCTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
 ATCATCACAAGGACAAGGGAAGTCAATCGACTAGTGGTGCGACGAATCGTC
 TACAGCAAAATTTATCAAAGTCAAGCTAATGCTTCATACAACCAACAATCT
 CAAGATTGGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
 ACAAAAAGCATTGAATGATCTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATGTATCCAGCTTCAAAAAGTCAAGTCAAGTA
 CTGTGTCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTTGGCTAATGTAAAAAAGACCAGGCTGTTAAATAAAAT
 CTAAGGTTCTATCCTGACAAGGAATGGGAAGGTAAATTTTCATATATCTCA
 AATTATCCAGAAGCAGAAGCAACAACCAATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTTATAAATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAAACAAGTTTACTGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTATTTGTTCTACAAGTTCTGTGACAAACAAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
 GGACAAATCGTAGTTACTAATCCAAGTAAAGCTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
 TG

SEQ ID NO. 8505

STRAIN 18RS21

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGAGTAAAACTAACTA
 CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
 AAAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCTACG
 ACACCTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTCTTC
 ATCATCACAAGGACAAGGGAAGTCAATCGACTAGTGGTGCGACGAATCGTC
 TACAGCAAAATTTATCAAAGTCAAGCTAATGCTTCATACAACCAACAATCT
 CAAGATTGGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
 ACAAAAAGCATTGAATGATGCTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATGTATCCAGCTTCAAAAAGTCAAGTCAAGTA
 CTGTGTCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTTGGCTAATGTAAAAAAGACCAGGCTGTTAAATAAAAT
 CTAAGGTTCTATCCTGACAAGGAATGGGAAGGTAAATTTTCATATATCTCA
 AATTATCCAGAAGCAGAAGCAACAACCAATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTTATAAATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAAACAAGTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTATTTGTCCTTACAAGTTCTGTGATAAACAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
 GGACAAATCGTGGTTACTAATCCAAGTAAACCTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAG

SEQ ID NO. 8506

STRAIN M732

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGAGTAAAACTAATTA
 CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
 AAAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCTACG
 ACACCTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAAACAGGGAGTTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
 ATCATCACAAGGACAAGGGAAGTCAATCGACTAGTGGTGCGACGAATCGTC
 TACAGCAAAATTTATCAAAGTCAAGCTAATGCTTCATACAACCAACAATCT
 CAAGATTGGAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
 ACAAAAAGCATTGAATGATGCTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATGTATCCAGCTTCAAAAAGTCAAGTCAAGTA
 CTGTGTCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTTGGCTAATGTAAAAAAGATCAGGCTGTTAAATAAAAT
 CTAAGGTTCTATCCTGACAAGGAATGGGAAGGTAAATTTTCATATATCTCA
 AATTATCCAGAAGCAGAAGCAACAACCAATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTTATAAATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAAACAAGTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTATTTGTCCTTACAAGTTCTGTGATAAACAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
 GGACAAATCGTGGTTACTAATCCAAGTAAACCTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
 TGAA

SEQ ID NO. 8507

STRAIN COH1

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGAGTAAAAAC
 TAATTACAAGTTTAAATGTTAGAGAAGGAAGTGTTCGTCTCAACTC
 TTTTGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTGAT
 GCTAATAAAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAAT
 CACAGCTGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAG
 CTTACGACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAAT
 AATCTAAAGACAAACAGGAGTTTTCAGCTATGGAATCAAGTGATCAATC

Table 85: Comparative Sequences relating to SAG1361

TTCATCATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGA
ATCGTCTACAGCAAAATTTATCAAAGTCAAGCTAATGCTTCATACAACCAA
CAACTTCAAGATTGAATGATGCTTATGCAGATGCACAGGCAGAAAGTAAA
TAAAGCACAAGGATGAATGATGCTTATTAACAAGTGACGTATCAG
GGACAGTTGTTGAAGTTAATAGTGATTTGATCCAGCTTCAAAAAGTAGT
CAAGTACTTGTCCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAAC
GATGAGTGAGTATGATTGGCTAATGTTAAAAAAGATCAGGCTGTTAAAA
TAAAACTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAAATTTATAT
ATCTCAAATTTATCCAGAAGCAGAAGCAACAACATGACTCTAATAACGG
CTCTAGTGTCTGTAATTTATAATATAAAGTAGATATTACTAGCCCTCTCG
ATGCATTAAAAACAGGTTTACCCTGATCAGTTGAAGTAGTTAATGGAGAT
AAGCACCTTATTGTCCCTACAAGTTCTGTGATAAACAAGATAATAAACA
CTTTGTTTGGGTATACAATGATTTCTAATCGTAAAAATTTCCAAGTTGAAG
TCAAAATTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTG
AAAGCAGGACAAATCGTGGTTACTAATCCAAGCAAACTTTCAAGGATGG
GCAAAAAATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAAT
CAGAGGTGAA

SEQ ID NO. 8507

STRAIN M781

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGAGTAAAACTAATTA
CAAGGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTTTGA
CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTTGATTTTGTATGCTAAT
AAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCACAGC
TGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAATAAAGTAGCGCTCAGATTAAATAATCTA
AAGACAACAGGGAGTTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
ATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAATCGTC
TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACCTT
CAAGATTTGAATGATGCTTATGTCAGATGCACAGGCAGAAAGTAAATAAAGC
ACAAAAGCATTGAATGATGCTTATTACAAGTGACGTATCAGGGACAG
TTGTTGAAGTTAATAGTGATTTGATCCAGCTTCAAAAAGTATGTTCAAGTA
CTTGTCCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
TGAGTATGATTTGGCTAATGTTAAAAAAGATCAGGCTGTTAAAAATAAAT
CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAAATTTATATATCTCA
AATTATCCAGAAGCAGAAGCAACAACAATGACTCTAATAACGGCTCTAG
TGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAAT
TAAACCAAGGTTTTACCCTGATCAGTTGAAGTAGTTAATGGAGATAAGCAC
CTTATTGTCCCTACAAGTTCTGTGATAAACAAGATAATAAACAACCTTGT
TTGGGTATACAATGATTTCTAATCGTAAAAATTTCCAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAGCA
GGACAAATCGTGGTTACTAATCCAAGCAAACTTTCAAGGATGGGCAAAA
AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
TGAA

SEQ ID NO. 8508

STRAIN CJB110

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGAGTAAAACTAATTA
CAAGGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTTTGA
CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTTGATTTTGTATGCTAAT
AAAGGTAATCGAGCAACTGTCACAGTTAAAGTGGGTGATAAAATCACAGC
TGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAATAAAGTAGCGCTCAGATTAAATAATCTA
AAGACAACAGGAAGTCTTCCAGCTATGGAATTAAGTGATCAATCTTCTTC
ATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAATCGTC
TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACCTT
CAAGATTTGAATGATGCTTATGTCAGATGCACAGGCAGAAAGTAAATAAAGC
ACAAAAGCATTGAATGATGCTTATTACAAGTGACGTATCAGGGACAG
TTGTTGAAGTTAATAGTGATTTGATCCAGCTTCAAAAAGTATGTTCAAGTA
CTTGTCCATGTAGCAACTGAAGGTAACTCCAAGTACAAGGAACGATGAG
TGAGTATGATTTGGCTAATGTTAAAAAAGACAGGCTGTTAAAAATAAAT
CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAAAAATTTATATATCTCA
AATTATCCAGAAGCAGAAGCAACAACAATGACTCTAATAACGGCTCTAG
TGCTGTAAATTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAAT
TAAACCAAGGTTTTACCCTGATCAGTTGAAGTAGTTAATGGAGATAAGCAC
CTTATTGTCCCTACAAGTTCTGTGATAAACAAGATAATAAACAACCTTGT
TTGGGTATACAATGATTTCTAATCGTAAAAATTTCCAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAGCA
GGACAAATCGTGGTTACTAATCCAAGTAAACCTTTCAAGGATGGGCAAAA
AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
TGA

SEQ ID NO. 8509

STRAIN 1169NT

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGAGTAAAACT
AACTACAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCT
TTTGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTTGATTTTGAATG
CTAATAAAGGTAATCGAGCAACTGTCACAGTTAAAGTGGGTGATAAAATC
ACAGCTGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGC
CTACGACACTGCTAATCGTCAATTAATAAAGTAGCGCTCAGATTAAATA
ATCTAAAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCT
TCTTCATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGAA
TCGCTCTACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAAC

Table 85: Comparative Sequences relating to SAG1361

AACTTCAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAAGTAAAT
 AAAGCACAAAAGCATTGAATGATCTGTTATTACAAGTGACGTATCAGG
 GACAGTTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAACAGTC
 AAGTACTTGTCCATGTAGCACTGAAGGTAACTCCAAGTACAAGGAACG
 ATGAGTGAGTATGATTTGGCTAATGTTAAAAAGACCAGGCTGTTAAAT
 AAAATCTAAGGTCTATCTGACAAGGAATGGGAAGGTAAATTTTATATA
 TCTCAAATTATCCAGAAGCAGAAGCAACAACTGACTCTAATAACGGC
 TCTAGTGTGTAATTTAATAATAAAGTAGATATTACTAGCCCTCTCGA
 TGCATTAAAACAAGGTTTACCGTATCAGTTGAAGTAGTTAATGGAGATA
 AGCACCTTATTGTCCCTACAAGTTCTGTGATAAACAAGATAATAACAC
 TTTGTTTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGT
 CAAAATTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGA
 AAGCAGGACAAATCGTGGTTACTAATCCAAGTAAACCTTCAAGGATGGG
 CAAAAAATTGATAATATTGAATCAATCGATCTTAACTCTAATAAGAAATC
 AGAGGTGAA

SEQ ID NO. 8510

STRAIN JM9130013

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAACTA
 CAAAGTTTAAATGTTAGAGAAGGAAGTGTTCGTCCCTCAACTCTTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGTATCTAAT
 AAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATACACAACCTGCACAAGCAGCCTACG
 ACATGCTAATCGTCAATTAATAAAGTAGCGCGTCAGATTAAATAATCTA
 AAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
 ATCATCACAAGGACAAGGGCTCAATCGACTAGTGGTGCGACGAATCGTC
 TACAGCAAAATTATCAAAGTCAAGCTAATGCTTCATACAACCAACAACTT
 CAAGATTGGAATGATGCTTATGCAGATGCACAGGCAGAAAGTAAATAAAGC
 ACAAAGAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
 TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAACTAGTCAAGTA
 CTTGTCCATGTAGCAACTGAGGTAAGTCCAAGTACAAGGAACGATGAG
 TGAGTATGATTGGCTAATGTTAAAAAGACCAGTCTGTTAAATAAATA
 CTAAGGTCTATCTGACAAGGAATGGGAAGGTAAATTTTATATATCTCA
 AATTATCCAGAAGCAGAAGCAACACAATGACTCTAATAACGGCTCTAG
 TGCTGTAAATTTAATAATAAAGTAGATATTACTAGCCCTCTCGATGCAT
 TAAAAACAAGGTTTACTGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATGTGTTCTTACAAGTTCTGTGACAAACAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
 TTGTTAAAGCTGATGCTTAAGACACAAGAAATTTTATCAGGTTTGAAGCA
 GGACAAATCGTGGTTACTAATCCAAGCAAACTTCAAGGATGGGCAAAA
 AATTGATAATATTGAATCAATAGATCTTAAAGTCTAATAAGAAATCAGAGG
 TGAAA

PRETTY of: /biotmp/msa363690.2{*} March 31, 2003 07:01 ..

	1						50
msa363690.2{690_COH1}	-----	-----	-----	-----	-----	-----	
msa363690.2{690_M732}	-----	-----	-----	-----	-----	-----	
msa363690.2{690_M781}	-----	-----	-----	-----	-----	-----	
msa363690.2{690_090}	-----	-----	-----	-----	-----	-----	
msa363690.2{690_CJB110}	-----	-----	-----	-----	-----	-----	
msa363690.2{690_1169NT}	-----	-----	-----	-----	-----	-----	
msa363690.2{690_18RS21}	-----	-----	-----	-----	-----	-----	
msa363690.2{690_2603}	atgagtaaac	gacaaaattt	aggaattagt	aaaaaaggag	caattatatac		
msa363690.2{690_A909}	-----	-----	-----	-----	-----	-----	
msa363690.2{690_JM9130013}	-----	-----	-----	-----	-----	-----	
msa363690.2{690_H36B}	-----	-----	-----	-----	-----	-----	
Consensus	*****	*****	*****	*****	*****	*****	

	51						100
msa363690.2{690_COH1}	-----	-----	-----	-----	TTT	TTATGGGTAC	
msa363690.2{690_M732}	-----	-----	-----	-----	TTT	TTATGGGTAC	
msa363690.2{690_M781}	-----	-----	-----	-----	TTT	TTATGGGTAC	
msa363690.2{690_090}	-----	-----	-----	-----	TTT	TTATGGGTAC	
msa363690.2{690_CJB110}	-----	-----	-----	-----	TTT	TTATGGGTAC	
msa363690.2{690_1169NT}	-----	-----	-----	-----	TTT	TTATGGGTAC	
msa363690.2{690_18RS21}	-----	-----	-----	-----	TTT	TTATGGGTAC	
msa363690.2{690_2603}	agggctctca	gtggcactaa	ttgtagtaat	aggtggcTTT	TTATGGGTAC		
msa363690.2{690_A909}	-----	-----	-----	-----	TTT	TTATGGGTAC	
msa363690.2{690_JM9130013}	-----	-----	-----	-----	TTT	TTATGGGTAC	
msa363690.2{690_H36B}	-----	-----	-----	-----	TTT	TTATGGGTAC	
Consensus	*****	*****	*****	*****	*****	*****	

	101						150
msa363690.2{690_COH1}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTTAAT		
msa363690.2{690_M732}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTTAAT		
msa363690.2{690_M781}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTTAAT		
msa363690.2{690_090}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTTAAT		
msa363690.2{690_CJB110}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTTAAT		
msa363690.2{690_1169NT}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTTAAT		
msa363690.2{690_18RS21}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTTAAT		
msa363690.2{690_2603}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTTAAT		

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_A909}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTAAAT
msa363690.2{690_JM9130013}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTAAAT
msa363690.2{690_H36B}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTAAAT
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	151	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	200
msa363690.2{690_M732}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_M781}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_090}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_CJB110}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_1169NT}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_18RS21}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_2603}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_A909}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_JM9130013}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_H36B}	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	201	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	250
msa363690.2{690_M732}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_M781}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_090}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_CJB110}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_1169NT}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_18RS21}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_2603}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_A909}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_JM9130013}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_H36B}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	251	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	300
msa363690.2{690_M732}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_M781}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_090}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_CJB110}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_1169NT}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_18RS21}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_2603}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_A909}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_JM9130013}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_H36B}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	301	GTTCAATATG	ATACAACAAC	TGCACAAGCA	350
msa363690.2{690_M732}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_M781}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_090}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_CJB110}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_1169NT}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_18RS21}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_2603}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_A909}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_JM9130013}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_H36B}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	351	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	400
msa363690.2{690_M732}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_M781}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_090}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_CJB110}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_1169NT}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_18RS21}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_2603}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_A909}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_JM9130013}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_H36B}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	401	GTtTTCCAGC	TATGGAATcA	AGTGATCAAT	450
msa363690.2{690_M732}	GTtTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA
msa363690.2{690_M781}	GTtTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA
msa363690.2{690_090}	GTtTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA
msa363690.2{690_CJB110}	GTtTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA
msa363690.2{690_1169NT}	GTtTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA
msa363690.2{690_18RS21}	GTtTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcATCATC	ATCACAAGGA

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_2603}	GTcTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTCtTCATC	ATCACAAGGA
msa363690.2{690_A909}	GTcTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTCaTCATC	ATCACAAGGA
msa363690.2{690_JM9130013}	GTcTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTCaTCATC	ATCACAAGGA
msa363690.2{690_H36B}	GTcTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTCaTCATC	ATCACAAGGA
Consensus	***-*****	*****-*	*****	*****-*****	*****
msa363690.2{690_COH1}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_M732}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_M781}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_090}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_CJB110}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_1169NT}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_18RS21}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_2603}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_A909}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_JM9130013}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_H36B}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
Consensus	*****-***	*****	*****	*****	*****
msa363690.2{690_COH1}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_M732}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_M781}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_090}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_CJB110}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_1169NT}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_18RS21}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_2603}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_A909}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_JM9130013}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
msa363690.2{690_H36B}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTTGAATG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_M732}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_M781}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_090}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_CJB110}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_1169NT}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_18RS21}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_2603}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_A909}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_JM9130013}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_H36B}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_M732}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_M781}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_090}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_CJB110}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_1169NT}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_18RS21}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_2603}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_A909}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_JM9130013}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_H36B}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_M732}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_M781}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_090}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_CJB110}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_1169NT}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_18RS21}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_2603}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_A909}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_JM9130013}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_H36B}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_M732}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_M781}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_090}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_CJB110}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_1169NT}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_18RS21}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_2603}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_A909}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_JM9130013}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_H36B}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
Consensus	*****-*	*****	*****	*****	*****
msa363690.2{690_COH1}	751	AAAAAGATCA	GgCTGTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_M732}	GCTAATGTtA	AAAAAGATCA	GgCTGTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_M781}	GCTAATGTtA	AAAAAGATCA	GgCTGTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_090}	GCTAATGTtA	AAAAAGATCA	GgCTGTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_CJB110}	GCTAATGTtA	AAAAAGATCA	GgCTGTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_1169NT}	GCTAATGTtA	AAAAAGATCA	GgCTGTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_18RS21}	GCTAATGTtA	AAAAAGATCA	GgCTGTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_2603}	GCTAATGTtA	AAAAAGATCA	GgCTGTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_A909}	GCTAATGTtA	AAAAAGATCA	GgCTGTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_JM9130013}	GCTAATGTtA	AAAAAGATCA	GgCTGTAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_H36B}	GCTAATGTtA	AAAAAGATCA	GgCTGTAA	ATAAAATCTA	AGGTCTATCC
Consensus	*****-*	*****	*-*****	*****	*****
msa363690.2{690_COH1}	801	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT
msa363690.2{690_M732}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_M781}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_090}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_CJB110}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_1169NT}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_18RS21}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_2603}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_A909}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_JM9130013}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_H36B}	TGACAAGGAA	TGGGAAGGTA	AAATTTTCATA	TATCTCAAAT	TATCCAGAAG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	851	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC
msa363690.2{690_M732}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_M781}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_090}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_CJB110}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_1169NT}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_18RS21}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_2603}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_A909}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_JM9130013}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
msa363690.2{690_H36B}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAATTTAT
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	901	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA
msa363690.2{690_M732}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_M781}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_090}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_CJB110}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_1169NT}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_18RS21}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_2603}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_A909}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_JM9130013}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_H36B}	AAATATAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTTT
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	951	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT
msa363690.2{690_M732}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_M781}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_090}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_CJB110}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_1169NT}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_18RS21}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_2603}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_A909}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_JM9130013}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_H36B}	TACcGTATCA	GTTGAAGTAG	TAAATGGAGA	TAAGCACCTT	ATTGTcCCTA
Consensus	***-*****	*****	*****	*****	*****
msa363690.2{690_COH1}	1001	CAAGTTCTGT	GatAAACAAA	GATAATAAAC	ACTTTGTTTG
msa363690.2{690_M732}	CAAGTTCTGT	GatAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAAT
msa363690.2{690_M781}	CAAGTTCTGT	GatAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAAT
msa363690.2{690_090}	CAAGTTCTGT	GatAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAAT
msa363690.2{690_CJB110}	CAAGTTCTGT	GatAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAAT

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_1169NT}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACITTTGTTTG	GGTATACAAT
msa363690.2{690_18RS21}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_2603}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_A909}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_JM9130013}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_H36B}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_M732}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_M781}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_090}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_CJB110}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_1169NT}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_18RS21}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_2603}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_A909}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_JM9130013}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_H36B}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_M732}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_M781}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_090}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_CJB110}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_1169NT}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_18RS21}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_2603}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_A909}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_JM9130013}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_H36B}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
Consensus	*****	*****	*****	*****	*****
msa363690.2{690_COH1}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_M732}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_M781}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_090}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_CJB110}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_1169NT}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_18RS21}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_2603}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_A909}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_JM9130013}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_H36B}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
Consensus	*****	***-***-*	*****	*****	*****
msa363690.2{690_COH1}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_M732}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_M781}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_090}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_CJB110}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_1169NT}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_18RS21}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_2603}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	aA
msa363690.2{690_A909}	GAATCAATaG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	aA
msa363690.2{690_JM9130013}	GAATCAATaG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	aA
msa363690.2{690_H36B}	GAATCAATcG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtg-	~
Consensus	*****	*****	*****	*****	---

SEQ ID NO. 8511

STRAIN 2603 frame: 1

MSKRQNLGI SKKGAIISGLSVALIVVIGGFLWVQS QPNKSAVKTNKYVFNVRREGSVSSST
 LLTGKAKANQEYVYFDANKGNRATVTVKVGDKITAGQQLVQYDTTAAQAYDTANRQLN
 KVARQINNLKTTGSLPAMESSDQSSSSSQGGTQSTSGATNRLQONYQS QANASYNQQLQ
 DLNDAYADAQAEVNKAQKALNDTVITSDVSGTVVEVNSDIDPASKTSQVLVHVATEGKLQ
 VQGTMSYDLANVKKDQAVKIKSKVYPDKWEWEGKISYISNYPEAEANNNDNNSSAVNY
 KYKVDITSPLDALKQGFVTSVEVNGDKHLIVPTSSVINKDNKHFVWVYNDNNRKRISKVE
 VKIGKADAKTQEILSGLKAGQIVVTNPSKTFKDGQKIDNIESIDLNSNKKSEVK

SEQ ID NO. 8512

STRAIN 090 frame: 1

FLWVQS QPNKSAVKTNKYVFNVRREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDTTAAQAYDTANRQLN KVARQINNLKTTGSLPAMESSDQSSSSSQ
 GGQTQSTSGATNRLQONYQS QANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSYDLANVKKDQAVKIKSKVYPDK
 EWEGKISYISNYPEAEANNNDNNSSAVNYKYKVDITSPLDALKQGFVTSVEVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNNRKRISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLNSNKKSE

Table 85: Comparative Sequences relating to SAG1361

SEQ ID NO. 8513

STRAIN A909 frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGAQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLVQVQGTMSSEYDLANVKKDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVTNKDNKHFWVYVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8514

STRAIN H36B frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLVQVQGTMSSEYDLANVKKDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVTNKDNKHFWVYVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 AFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8515

STRAIN 18RS21 frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLVQVQGTMSSEYDLANVKKDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFWVYVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLNSNKKSE

SEQ ID NO. 8516

STRAIN M732 frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLVQVQGTMSSEYDLANVKKDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFWVYVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8517

STRAIN COH1 frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLVQVQGTMSSEYDLANVKKDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFWVYVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8518

STRAIN M781 frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLVQVQGTMSSEYDLANVKKDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFWVYVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8519

STRAIN M781 frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLVQVQGTMSSEYDLANVKKDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFWVYVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8520

STRAIN CJB110 frame: 1

FLWVQSQPNKSAVKTNKYKFNVRREGSVSSSTLLTGKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQVLVHVATEGKLVQVQGTMSSEYDLANVKKDQAVKI KSKVYPDK
 EWEGKISYI SNYPEAEANNNDSNNGSSAVNYKYKVDITSPDLALKQGFVTSVEVVNGDKH
 LIVPTSSVINKDNKHFWVYVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLNSNKKSEV

SEQ ID NO. 8521

Table 85: Comparative Sequences relating to SAG1361

STRAIN 1169NT frame: 1

FLWVQSQPNKSAVKTNKYVFNREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAAQAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGTQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVEVNSDIDPASKTSQVLHVHATEGKLVQVQGTMSYDLANVKKDQAVKI KSKVYPPDK
 EWEGKISYISNYPEAEANNDNSNGSSAVNYKYKVDITSPLDALKQGFTVSVEVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TPKDGQKIDNIESIDLNSNKKSEV

SEQ ID NO. 8522

STRAIN JM9130013 frame: 1

FLWVQSQPNKSAVKTNKYVFNREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTTAAQAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQ
 GQGAQSTSGATNRLQNNYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVEVNSDIDPASKTSQVLHVHATEGKLVQVQGTMSYDLANVKKDQAVKI KSKVYPPDK
 EWEGKISYISNYPEAEANNDNSNGSSAVNYKYKVDITSPLDALKQGFTVSVEVNGDKH
 LIVPTSSVINKDNKHFVWVYNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TPKDGQKIDNIESIDLNSNKKSEV

PRETTY of: /biotmp/msa375805.2{*} April 1, 2003 02:58 ..

	1		50
msa375805.2{690_COH1}	-----	-----	-----F LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_M732}	-----	-----	-----F LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_M781}	-----	-----	-----F LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_090}	-----	-----	-----F LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_CJB110}	-----	-----	-----F LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_1169NT}	-----	-----	-----F LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_18RS21}	-----	-----	-----F LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_2603}	mskrqnlgis	kggaiisgls	valivviggF LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_A909}	-----	-----	-----F LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_JM9130013}	-----	-----	-----F LWVQSQPNKS AVKTNKYVFN
msa375805.2{690_H36B}	-----	-----	-----F LWVQSQPNKS AVKTNKYVFN
Consensus	*****	*****	*****
	51		100
msa375805.2{690_COH1}	VREGSVSSST	LLTGKAKANQ	EQVYVFDANK GNRATVTVKV GDKITAGQQL
msa375805.2{690_M732}	VREGSVSSST	LLTGKAKANQ	EQVYVFDANK GNRATVTVKV GDKITAGQQL
msa375805.2{690_M781}	VREGSVSSST	LLTGKAKANQ	EQVYVFDANK GNRATVTVKV GDKITAGQQL
msa375805.2{690_090}	VREGSVSSST	LLTGKAKANQ	EQVYVFDANK GNRATVTVKV GDKITAGQQL
msa375805.2{690_CJB110}	VREGSVSSST	LLTGKAKANQ	EQVYVFDANK GNRATVTVKV GDKITAGQQL
msa375805.2{690_1169NT}	VREGSVSSST	LLTGKAKANQ	EQVYVFDANK GNRATVTVKV GDKITAGQQL
msa375805.2{690_18RS21}	VREGSVSSST	LLTGKAKANQ	EQVYVFDANK GNRATVTVKV GDKITAGQQL
msa375805.2{690_2603}	VREGSVSSST	LLTGKAKANQ	EQVYVFDANK GNRATVTVKV GDKITAGQQL
msa375805.2{690_A909}	VREGSVSSST	LLTGKAKANQ	EQVYVFDANK GNRATVTVKV GDKITAGQQL
msa375805.2{690_JM9130013}	VREGSVSSST	LLTGKAKANQ	EQVYVFDANK GNRATVTVKV GDKITAGQQL
msa375805.2{690_H36B}	VREGSVSSST	LLTGKAKANQ	EQVYVFDANK GNRATVTVKV GDKITAGQQL
Consensus	*****	*****	*****
	101		150
msa375805.2{690_COH1}	VQYDITTTAAQ	AYDTANRQLN	KVARQINNLTGSLPAMEs SDQSSSSSQ
msa375805.2{690_M732}	VQYDITTTAAQ	AYDTANRQLN	KVARQINNLTGSLPAMEs SDQSSSSSQ
msa375805.2{690_M781}	VQYDITTTAAQ	AYDTANRQLN	KVARQINNLTGSLPAMEs SDQSSSSSQ
msa375805.2{690_090}	VQYDITTTAAQ	AYDTANRQLN	KVARQINNLTGSLPAMEs SDQSSSSSQ
msa375805.2{690_CJB110}	VQYDITTTAAQ	AYDTANRQLN	KVARQINNLTGSLPAMEs SDQSSSSSQ
msa375805.2{690_1169NT}	VQYDITTTAAQ	AYDTANRQLN	KVARQINNLTGSLPAMEs SDQSSSSSQ
msa375805.2{690_18RS21}	VQYDITTTAAQ	AYDTANRQLN	KVARQINNLTGSLPAMEs SDQSSSSSQ
msa375805.2{690_2603}	VQYDITTTAAQ	AYDTANRQLN	KVARQINNLTGSLPAMEs SDQSSSSSQ
msa375805.2{690_A909}	VQYDITTTAAQ	AYDTANRQLN	KVARQINNLTGSLPAMEs SDQSSSSSQ
msa375805.2{690_JM9130013}	VQYDITTTAAQ	AYDTANRQLN	KVARQINNLTGSLPAMEs SDQSSSSSQ
msa375805.2{690_H36B}	VQYDITTTAAQ	AYDTANRQLN	KVARQINNLTGSLPAMEs SDQSSSSSQ
Consensus	*****	*****	*****
	151		200
msa375805.2{690_COH1}	QGTQSTSGAT	NRLQNNYQSQ	ANASYNQQLQ DLNDAYADAQ AEVNKAQKAL
msa375805.2{690_M732}	QGTQSTSGAT	NRLQNNYQSQ	ANASYNQQLQ DLNDAYADAQ AEVNKAQKAL
msa375805.2{690_M781}	QGTQSTSGAT	NRLQNNYQSQ	ANASYNQQLQ DLNDAYADAQ AEVNKAQKAL
msa375805.2{690_090}	QGTQSTSGAT	NRLQNNYQSQ	ANASYNQQLQ DLNDAYADAQ AEVNKAQKAL
msa375805.2{690_CJB110}	QGTQSTSGAT	NRLQNNYQSQ	ANASYNQQLQ DLNDAYADAQ AEVNKAQKAL
msa375805.2{690_1169NT}	QGTQSTSGAT	NRLQNNYQSQ	ANASYNQQLQ DLNDAYADAQ AEVNKAQKAL
msa375805.2{690_18RS21}	QGTQSTSGAT	NRLQNNYQSQ	ANASYNQQLQ DLNDAYADAQ AEVNKAQKAL
msa375805.2{690_2603}	QGTQSTSGAT	NRLQNNYQSQ	ANASYNQQLQ DLNDAYADAQ AEVNKAQKAL
msa375805.2{690_A909}	QGTQSTSGAT	NRLQNNYQSQ	ANASYNQQLQ DLNDAYADAQ AEVNKAQKAL
msa375805.2{690_JM9130013}	QGTQSTSGAT	NRLQNNYQSQ	ANASYNQQLQ DLNDAYADAQ AEVNKAQKAL
msa375805.2{690_H36B}	QGTQSTSGAT	NRLQNNYQSQ	ANASYNQQLQ DLNDAYADAQ AEVNKAQKAL
Consensus	***-*****	*****	*****
	201		250
msa375805.2{690_COH1}	NDTVITSDVS	GTVEVNSDI	DPASKTSQVL VHVATEGKLQ VQGTMSYDL
msa375805.2{690_M732}	NDTVITSDVS	GTVEVNSDI	DPASKTSQVL VHVATEGKLQ VQGTMSYDL
msa375805.2{690_M781}	NDTVITSDVS	GTVEVNSDI	DPASKTSQVL VHVATEGKLQ VQGTMSYDL
msa375805.2{690_090}	NDTVITSDVS	GTVEVNSDI	DPASKTSQVL VHVATEGKLQ VQGTMSYDL

Table 85: Comparative Sequences relating to SAG1361

msa375805.2{690_CJB110}	NDTVITSDVS	GTVEVNDSI	DPASKTSQVL	VHVATEGKLQ	VQGTMSSEYDL
msa375805.2{690_1169NT}	NDTVITSDVS	GTVEVNDSI	DPASKTSQVL	VHVATEGKLQ	VQGTMSSEYDL
msa375805.2{690_18RS21}	NDTVITSDVS	GTVEVNDSI	DPASKTSQVL	VHVATEGKLQ	VQGTMSSEYDL
msa375805.2{690_2603}	NDTVITSDVS	GTVEVNDSI	DPASKTSQVL	VHVATEGKLQ	VQGTMSSEYDL
msa375805.2{690_A909}	NDTVITSDVS	GTVEVNDSI	DPASKTSQVL	VHVATEGKLQ	VQGTMSSEYDL
msa375805.2{690_JM9130013}	NDTVITSDVS	GTVEVNDSI	DPASKTSQVL	VHVATEGKLQ	VQGTMSSEYDL
msa375805.2{690_H36B}	NDTVITSDVS	GTVEVNDSI	DPASKTSQVL	VHVATEGKLQ	VQGTMSSEYDL
Consensus	*****	*****	*****	*****	*****
	251				300
msa375805.2{690_COH1}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_M732}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_M781}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_090}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_CJB110}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_1169NT}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_18RS21}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_2603}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_A909}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_JM9130013}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_H36B}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
Consensus	*****	*****	*****	*****	*****
	301				350
msa375805.2{690_COH1}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSViNK	DNKHFVWVYN
msa375805.2{690_M732}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSViNK	DNKHFVWVYN
msa375805.2{690_M781}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSViNK	DNKHFVWVYN
msa375805.2{690_090}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSViNK	DNKHFVWVYN
msa375805.2{690_CJB110}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSViNK	DNKHFVWVYN
msa375805.2{690_1169NT}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSViNK	DNKHFVWVYN
msa375805.2{690_18RS21}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSViNK	DNKHFVWVYN
msa375805.2{690_2603}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSViNK	DNKHFVWVYN
msa375805.2{690_A909}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSViNK	DNKHFVWVYN
msa375805.2{690_JM9130013}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSViNK	DNKHFVWVYN
msa375805.2{690_H36B}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSViNK	DNKHFVWVYN
Consensus	*****	*****	*****	*****	*****
	351				400
msa375805.2{690_COH1}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKt	FKDGQKIDNI
msa375805.2{690_M732}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKt	FKDGQKIDNI
msa375805.2{690_M781}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKt	FKDGQKIDNI
msa375805.2{690_090}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKt	FKDGQKIDNI
msa375805.2{690_CJB110}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKt	FKDGQKIDNI
msa375805.2{690_1169NT}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKt	FKDGQKIDNI
msa375805.2{690_18RS21}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKt	FKDGQKIDNI
msa375805.2{690_2603}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKt	FKDGQKIDNI
msa375805.2{690_A909}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKt	FKDGQKIDNI
msa375805.2{690_JM9130013}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKt	FKDGQKIDNI
msa375805.2{690_H36B}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKa	FKDGQKIDNI
Consensus	*****	*****	*****	*****	*****
	401				414
msa375805.2{690_COH1}	ESIDLkSNKK	SEv-			
msa375805.2{690_M732}	ESIDLkSNKK	SEv-			
msa375805.2{690_M781}	ESIDLkSNKK	SEv-			
msa375805.2{690_090}	ESIDLnSNKK	SE--			
msa375805.2{690_CJB110}	ESIDLnSNKK	SEv-			
msa375805.2{690_1169NT}	ESIDLnSNKK	SEv-			
msa375805.2{690_18RS21}	ESIDLnSNKK	SE--			
msa375805.2{690_2603}	ESIDLnSNKK	SEvK			
msa375805.2{690_A909}	ESIDLkSNKK	SEvK			
msa375805.2{690_JM9130013}	ESIDLkSNKK	SEvK			
msa375805.2{690_H36B}	ESIDLkSNKK	SEv-			
Consensus	*****	***			

Table 86: Comparative Sequences relating to SAG1393

SEQ ID NO. 8601

STRAIN 2603

atgaaaaaattggaattattgtcctcacactactgacctcttttttggtatcttgcgga
 caacaaactaaacaagaaagcactaaaacaactatttctaaaatgcctaaaattgaaggc
 ttcacctattatggaaaaattcctgaaaatccgaaaaagtaattatttacatatctt
 tacactgggtattttataaaactaggtgttaattgttcaagttacagtttagacttagaa
 aaagatagcccggttttttggttaaacacactgaaagaagctaaaaaattactgctgatgat
 acagaagctattgcccgcacaaaaacctgatttaatacatggttttcgatcaagatccaaac
 atcaatactctgaaaaaaattgcaccaactttagttatataatattggtgcacaaaattat
 ttagatatgatgccagccttggggaaagattcggtaaagaaaaagaagctaatacagtggtg
 gttagccaattggaaaaactaaaactctcgctgtcaaaaaagatttaacaccatatcttaag
 cctaacactacttttactattatggatttttatgataaaaaatctattttatattggtaat
 aattttggacgggtggagaactaatctatgattcactaggttatgctgccccagaaaaa
 gtcaaaaaagatgtcttttaaaaaagggtggtttaccgtttcgcaagaagcaatcggtgat
 tacgttggagattatgcccttgttaataataacaaaacgactaaaaagcagcttcatca
 cttaagaaagtgatgtctggaagaatttaccagctgtcaaaaaagggcacatcatagaa
 agtaactacgagctgttttatttctctgacctctatctttagaagctcaattaaaatca
 tttacaaaggctatcaagaaaaatacaaat

SEQ ID NO. 8602

STRAIN 090

GAAGGCTTCACCTATTATGGAAAAATTCCTGAAAAATCCGAAAAAGTAAT
 TAATTTTACATATTCTTACACTGGGTATTTATTAATACTAGGTGTTAATG
 TTTCAAGTTACAGTTTAGACTTAGAAAAAGATAGCCCCGTTTTTGGTAAAG
 CAACTGAAAGAGCTAAAAAATTAAC'TGCTGATGATACAGAAGCTATTGTC
 CGCACAAAAACCTGATTTAATCATGGTTTTCGATCAAGATCCAAACATCA
 ATACTCTGAAAAAAATTCACCAACTTTAGTTATTAATATGGTGCACAA
 AATTATTTAGATATGATGCCAGCCTTGGGAAAGTATTCGGTAAAGAAAA
 AGAAGCTAATCAGTGGGTTAGCCAATGGAAAACTAAAACTCTCGCTGCCA
 AAAAAAGATTTACCATATCTTAAAGCCTAACACTACTTTTACTATTATG
 GATTTTATGATAAAAAATATCTATTTATATGGTAATAATTTTGGACGGG
 TGGAGAACTAATCTATGATTCAGTGGTTATGCTGCCCAgAAAAAGTCA
 AAAAAgATGTcTTTAAAAAAGGGTGGTTTACCCTTTTCgCAAGAAGCAATC
 GGTGATTACGTTGGAGATTATGCCCTTGTTAATATAAACAACGACTAA
 AAAAGCAGCTTCatcACTTAAAGAAAGTGATGTCTGGAAGAAATTTACCAG
 CTGTcAAAAAAGGGCACATCATAGAAAGTAacTACGACGTGTTTTATTTC
 TCTGACCTCTATCTTTTAGAAGCTCAATTAAAAATCATTTACAAA

SEQ ID NO. 8603

STRAIN A909

GAAGGCTTCACCTATTATGGAAAAATTCCTG
 AAAATCCGAAAAAGTAATTAATTTTACATATTCTTACACTGGATATTTA
 TTAAACTAGGAGTTAATGTTTCAAGTTACAGTTTAGACTTAGAAAAAGA
 TAgCCCCGTTTTTGGTAAaCAACTGAAAGGAGCTAAAAAATTAAC'TGCTG
 ATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAaTCATGGTTTTT
 GATCAAGATCCAAACATCAATACTCTGAAAAAATTCACCAACTTTTAGT
 TATTAATATGGTGACAAAAATTTTATagAtaTGATGCCAGCTTTGGGGA
 AAGTATTCGGTAAAGAAAAAGAGCTAATCAGTGGGTTAGCCAaTGGAAA
 ACTAAAACTCTCGCTGCCAAAAAAGATTACACCATATCTTAAACCTAA
 CACTACTTTTACCATTATGGATTTTATGATAAAAAATATCTATTTATATG
 GTAATAATTTTGGACGGGTGGAGAATAATCTATGATTCAGTGGTTAT
 GCTGCCCCAGAAAAAGTCAAAAAAGATGCTTTTAAAAAAGGGTGGTTTAC
 CGTTTCGCAAGAAAGCAATCGGTgATTACGTTGGAGATTATGCCCTTGTTA
 ATATAAACAACGACTAAAAAAGCAGCTTCATCACTTAAAGAAAGTGAT
 GTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATCATAGAAAGTAA
 CTACGACGTGTTTTATTCTCTGACCCTcTATCTTTAGAAGCTCAATTAA
 AATCATTTACAAA

SEQ ID NO. 8604

STRAIN H36B

GAAGGCTTCACCTATTATGGAAAA
 ATTCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACACTGG
 ATATTTATTAAAACTAGGAGTTAATGTTTCAAGTTACAGTTTAGACTTAG
 AAAAAAGATAgCCCCGTTTTTGGTAAgCAACTGAAAGGAGCTAAAAAATTA
 ACTGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAaTCAT
 GGTTTTTGATCAAgATCCAAACATCAATACTCTGAAAAAATTCACCAA
 CTTTAGTTATTAAATATGGTGACAAAATTTTATagAtaTGATGCCAGCT
 TTGGGGAaAGTATTCGGTAAAGAAAAAGAGCTAATCAGTGGGTTAGCCA
 ATGGAAAACTAAAACTCTCGCTGCCAAAAAAGATTACACCATATCTTAA
 GGCTTaCAcACTTTTACTATTATAGatTTTATGATAAAAAATATCTAT
 TTTATATGGTAATAATTTTGGACGGGTGGAgAACTAATCTATGATcCACT
 AGGTTATGCTGCCCAgAAAAAGTCAAAAAAgATGTCTTTAAAAAAGGGT
 GGTTTACCCTTTTCgCAAGAAGCAATCGGTgATTACGTTGGAGATTATGCC
 CTTGTTAATATAAACAACGACTAAAAAAGCAGCTTCaTCACTTAAAGA
 AAGTGATGTTTGGAGAATTTACCAGCTGTCAAAAAAGGGCACATCATAG
 AAAGTAACACGAGCTGTTTTATTCTCTGACCCTCTATCTTTAGAAGCT
 CAATTAAATCATTTACAAA

Table 86: Comparative Sequences relating to SAG1393

SEQ ID NO. 8605

STRAIN 18RS21

GAAGGCTTCACCTATTATGGA
 AAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACAC
 TGGGTATTTATTAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAGACT
 TAGAAAAAGATAGCCCCGTTTTTGGTAAACAACTGAAAGAAGCTAAAAAA
 TTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAAT
 CATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCAC
 CAACCTTAGTTATTAAATATGGTGCACAAAATTATTTAgATaTGATGCCA
 GCCTTGGGGAAAGTATTTCGGTAAAGAAAAgAAGCTAATCAGTGGGTTAG
 CCAATGGAAAACTAAAACTCTCGCTGTCAAAAAAGATTACACCATATCT
 TAAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAAATATC
 TATTTATATGTTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATTCT
 ACTAGGTTATGCTGCCCCagAAAAAGTCAAAAAgATGTCTTTAAAAAAG
 GGTGGTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTAT
 GCCCTTGTTAATATAAAACAAACgACTAAAAAGCAGCTTCATCACTTAA
 AGAAAGTGATGTCTGGAAGAATTACCAGCTGTCAAAAAAGGGCACATCA
 TAGAAAGTAACTACGACGTGTTTTATTCTCTGACCCTCTATCTTTAGAA
 GCTCAATTAAATCATTACAAA

SEQ ID NO. 8606

STRAIN M732

GAAGGCTTCACCTATTATGG
 AAAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACA
 CTGGGTATTTATTAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAGAC
 TTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAA
 ATTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTAA
 TCATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCA
 CCACTTTAGTTATTAAATATGGTGCACAAAATTATTTAgATaTGATGCC
 AGCCTTGGGGAAAGTATTTCGGTAAAGAAAAAGAGCTAATCAGTGGGTTA
 GCCAATGGAAAACTAAAACTCTCGCTGCCAAAAAGATTACACCATATC
 TTAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAAATAT
 CTATTTATATGGTAATAATTTTGGACgCGGTGGAGAACTAATCTATGATT
 CACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAA
 GGGTGGTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTA
 TGCCCTTGTTAATATAAAACAAACGACTAAAAAGCAGCTTCATCACTTA
 AAGAAAGTGATGTCTGGAAGAATTACCAGCTGTCAAAAAAGGGCACATC
 ATAGAAAGTAACTACGACGTGTTTTATTCTCTGACCCTCTATCTTTAGA
 AGCTCAATTAAATCATTACAAA

SEQ ID NO. 8607

STRAIN COH1

GAAGGCTTCACCTATTATG
 GAAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTAC
 ACTGGGTATTTATTAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAgA
 CTTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAA
 AATTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTAA
 ATCATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGC
 ACCAATTTAGTTATTAAATATGGTGCACAAAATTATTTAgATaTGATGC
 CAGCCTTGGGGAAAGTaTTcGGTAAAGAAAAAGAGCTAATCAGTGGGTT
 AGCCAATGGAAAACTAAAACTCTCGCTGCCAAAAAGATTACACCATAT
 CTTAAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAAATA
 TCTATTTATATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGAT
 TCCTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAA
 AGGGTGGTTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATT
 ATGCCCTTGTTAATATAAAACAAACGACTAAAAAGCAGCTTCATCACTT
 AAAGAAAGTGATGTCTGGAAGAATTACCAGCTGTCAAAAAAGGGCACAT
 CATAGAAAGTAACTACGACGTGTTTTATTCTCTGACCCTCTATCTTTAG
 AAGCTCAATTAAATCATTACAAA

SEQ ID NO. 8608

STRAIN M781

GAAGGCTTCACCTATTATGG
 AAAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACA
 CTGGGTATTTATTAAACTAGGTGTTAATGTTTCAAGTTACAGTTTAGAC
 TTAgAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAA
 ATTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTAA
 TCATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAAATTGCA
 CCACTTTAGTTATTAAATATGGTGCACAAAATTATTTAgATaTGATGCC
 AGCCTTGGGGAAAGTATTTCGGTAAAGAAAAAGAGCTAATCAGTGGGTTA
 GCCAATGGAAAACTAAAACTCTCGCTGCCAAAAAGATTACACCATATC
 TTAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAAATAT
 CTATTTATATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATT
 CACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAA
 GGGTGGTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTA
 TGCCCTTGTTAATATAAAACAAACGACTAAAAAGCAGCTTCATCACTTA

Table 86: Comparative Sequences relating to SAG1393

AAGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAGGGCACATC
 ATAGAAAGTAACACGACGTGTTTATTCTCTGACCCCTCTATCTTTAGA
 AGCTCAATTAATAATCATTACAAA

SEQ ID NO. 8609

STRAIN CJB110

GAAGGCTTCACCTATTATGGA

AAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACAC
 TGGGTATTTATTAATACTAGGTGTTAATGTTTCAAGTTACAGTTTAGACT
 TAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAAA
 TTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAACCTGATTTAAT
 CATGGTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAATTGCAC
 CAACTTTAGTTATTAATATGGTGCACAAAATTATTTAgATATGATGCCA
 GCCTTGGGGAAGTATTCGGTAAAGAAAAAGAGCTAATCAGTGGGTAG
 CCAATGGAAAACTAAACTCTCGCTGCCAAAAAGATTACACCATATCT
 TAAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAATATC
 TATTTATATGTTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATTC
 ACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAGATGCTTTAAAAAAG
 GGTGGTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTAT
 GCCCTTGTTAATATAACAAAACGACTAAAAAAGCAGCTTCATCACTTAA
 AGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAGGGCACATCA
 TAGAAAGTAACACGACGTGTTTATTCTCTGACCCCTCTATCTTTAGAA
 GCTCAATTAATAATCATTACAAA

SEQ ID NO. 8610

STRAIN 1169NT

GAAGGCTTCACCTATTATGGAATAAT

CCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACACTGGGTA
 TTTATTAATACTAGGTGTTAATGTTTCAAGTTACAGTTTAGACTTAGAAA
 AAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAAATTAAT
 GCTGATGATACAGAAGCTATTGCCGcACAAaaACCTGATTTAATCATGGT
 TTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAATTGCACCAACTT
 TAGTTATTAATAATATGGTGCACAAAATTTATTTAgATATGATGCCAGCCTTG
 GGGAAAGTATTCGGTAAAGAAAAAGaaGCTAATCAGTGGGTTAGCCAATG
 GAAAACTAAACTCTCGCTGCCAAAAAGATTACACCATATCTTAAAGC
 CTAACACTACTTTTACTATTATGGATTTTTATGATAAAAATATCTATTTA
 TATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATTCAC TAGG
 TTATGCTGCCCAgAAAAAGTCAAAAAGATGCTTTAAAAAAGGGTGGT
 TTACCGTTTTcGCAAGAAGCAATCGGTGATTACGTTGGAGATTATGCCCTT
 GTTAATATAAACAACGACTAAAAAAGCAGCTTCATCACTTAAAGAAAG
 TGATGTCTGGAAGAATTTACCAGCTGTCAAAAAGGGCACATCATAGAAA
 GTAACACGACGTGTTTATTCTCTGACCCCTCTATCTTTAGAAGCTCAA
 TTAAATCATTACAAA

SEQ ID NO. 8611

STRAIN JM9130013

GAAGGCTTCACCTATTATG

GAAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTAC
 ACTGATATTATTAACTAGGAGTTAATGTTTCAAGTTACAGTTTAGA
 CTTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGGAGCTAAAA
 AATTAACGTCTGATGATACAGAAGCTATTGCCGCACAAAACCTGATTTA
 ATCATGGTTTTGATCAAGATCCAAACATCAATACTCTGAAAAAATTGTC
 ACCAACTTTAGTTATTAATAATGGTGCACAAAATTATTTAgATATGATGC
 CAGCTTTGGGGAAGTATTCGGTAAAGAAAAAGAGCTAATCAGTGGGTT
 AGCCAATGGAAAACTAAACTCTCGCTGCCAAAAAGATTACACCATAT
 CTTAAACCTTAACACTACTTTTACCATTATGGATTTTTATGATAAAAATA
 TCTATTTATATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGAT
 TCAC TAGGTTATGCTGCCCAgAAAAAGTCAAAAAGATGCTTTAAAAA
 AGGGTGGTTTACCGTTTTcGCAAGAAGCAATCGGTGATTACGTTGGAGATT
 ATGCCCTTGTTAATATAAACAACGACTAAAAAAGCAGCTTCATCACTT
 AAAGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAGGGCACAT
 CATAGAAAGTAACACGACGTGTTTATTCTCTGACCCCTCTATCTTTAG
 AAGCTCAATTAATAATCATTACAAA

PRETTY of: /biotmp/msa521731.2{*} April 28, 2003 08:07 ..

	1	50
msa521731.2{691_090}	-----	-----
msa521731.2{691_1169NT}	-----	-----
msa521731.2{691_CJB110}	-----	-----
msa521731.2{691_COH1}	-----	-----
msa521731.2{691_M732}	-----	-----
msa521731.2{691_M781}	-----	-----
msa521731.2{691_18RS21}	-----	-----
msa521731.2{691_2603}	atgaaaaaaa	ttggaattat tgtcctcaca ctactgacct tctttttggt

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_A909}	-----	-----	-----	-----	-----
msa521731.2{691_JM9130013}	-----	-----	-----	-----	-----
msa521731.2{691_H36B}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa521731.2{691_090}	-----	-----	-----	-----	-----
msa521731.2{691_1169NT}	-----	-----	-----	-----	-----
msa521731.2{691_CJB110}	-----	-----	-----	-----	-----
msa521731.2{691_COH1}	-----	-----	-----	-----	-----
msa521731.2{691_M732}	-----	-----	-----	-----	-----
msa521731.2{691_M781}	-----	-----	-----	-----	-----
msa521731.2{691_18RS21}	-----	-----	-----	-----	-----
msa521731.2{691_2603}	atcttgcgga	caacaaacta	aacaagaaag	cactaaaaca	actatttcta
msa521731.2{691_A909}	-----	-----	-----	-----	-----
msa521731.2{691_JM9130013}	-----	-----	-----	-----	-----
msa521731.2{691_H36B}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	101				150
msa521731.2{691_090}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_1169NT}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_CJB110}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_COH1}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_M732}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_M781}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_18RS21}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_2603}	aaatgcctaa	aattGAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_A909}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_JM9130013}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_H36B}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
Consensus	*****	*****	*****	*****	*****
	151				200
msa521731.2{691_090}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_1169NT}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_CJB110}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_COH1}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_M732}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_M781}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_18RS21}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_2603}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_A909}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_JM9130013}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_H36B}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
Consensus	*****	*****	*****	*****	*****
	201				250
msa521731.2{691_090}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_1169NT}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_CJB110}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_COH1}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_M732}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_M781}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_18RS21}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_2603}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_A909}	ACTAGGaGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_JM9130013}	ACTAGGaGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_H36B}	ACTAGGaGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
Consensus	*****	*****	*****	*****	*****
	251				300
msa521731.2{691_090}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_1169NT}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_CJB110}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_COH1}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_M732}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_M781}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_18RS21}	CCGTTTTTGG	TAAaCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_2603}	CCGTTTTTGG	TAAaCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_A909}	CCGTTTTTGG	TAAaCAACTG	AAAGgAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_JM9130013}	CCGTTTTTGG	TAAgCAACTG	AAAGgAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_H36B}	CCGTTTTTGG	TAAgCAACTG	AAAGgAGCTA	AAAAATTAAC	TGCTGATGAT
Consensus	*****	***-*****	*****	*****	*****
	301				350
msa521731.2{691_090}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_1169NT}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_CJB110}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_COH1}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_M732}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_M781}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_18RS21}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_2603}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_A909}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_JM9130013}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_H36B}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
Consensus	*****	*****	*****	*****	*****
msa521731.2{691_090}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_1169NT}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_CJB110}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_COH1}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_M732}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_M781}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_18RS21}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_2603}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_A909}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_JM9130013}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_H36B}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
Consensus	*****	*****	*****	*****	*****
msa521731.2{691_090}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_1169NT}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_CJB110}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_COH1}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_M732}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_M781}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_18RS21}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_2603}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_A909}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_JM9130013}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
msa521731.2{691_H36B}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCCTT	GGGGAAAGTA
Consensus	*****	*****	*****	*****	*****
msa521731.2{691_090}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_1169NT}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_CJB110}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_COH1}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_M732}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_M781}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_18RS21}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_2603}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_A909}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_JM9130013}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
msa521731.2{691_H36B}	TTTCGGTAAAG	AAAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACTAA
Consensus	*****	*****	*****	*****	*****
msa521731.2{691_090}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_1169NT}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_CJB110}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_COH1}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_M732}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_M781}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_18RS21}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_2603}	AACTCTCGCT	GtCAAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_A909}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAaa	CCTAACACTA
msa521731.2{691_JM9130013}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAaa	CCTAACACTA
msa521731.2{691_H36B}	AACTCTCGCT	GcCAAAAAAG	ATTTACACCA	TATCTTAAgg	CCTAACACTA
Consensus	*****	*-*****	*****	*****	*****
msa521731.2{691_090}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_1169NT}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_CJB110}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_COH1}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_M732}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_M781}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_18RS21}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_2603}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_A909}	CTTTTACCAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_JM9130013}	CTTTTACCAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_H36B}	CTTTTACTAT	TATaGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
Consensus	*****_**	***-*****	*****	*****	*****
	601				650
msa521731.2{691_090}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_1169NT}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_CJB110}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_COH1}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_M732}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_M781}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_18RS21}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_2603}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_A909}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_JM9130013}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_H36B}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
Consensus	*****	*****	*****	*****	*****
	651				700
msa521731.2{691_090}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_1169NT}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_CJB110}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_COH1}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_M732}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_M781}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_18RS21}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_2603}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_A909}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_JM9130013}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_H36B}	CCCAGAAAAA	GTCAAAAAAG	ATGTCTTTAA	AAAAGGGTGG	TTTACCGTTT
Consensus	*****	*****	*****	*****	*****
	701				750
msa521731.2{691_090}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_1169NT}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_CJB110}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_COH1}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_M732}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_M781}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_18RS21}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_2603}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_A909}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_JM9130013}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_H36B}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
Consensus	*****	*****	*****	*****	*****
	751				800
msa521731.2{691_090}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_1169NT}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_CJB110}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_COH1}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_M732}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_M781}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_18RS21}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_2603}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_A909}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_JM9130013}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_H36B}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
Consensus	*****	*****	*****	*****	*****_**
	801				850
msa521731.2{691_090}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_1169NT}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_CJB110}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_COH1}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_M732}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_M781}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_18RS21}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_2603}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_A909}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_JM9130013}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_H36B}	GAAGAATTTA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA	AGTAACTACG
Consensus	*****	*****	*****	*****	*****
	851				900
msa521731.2{691_090}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_1169NT}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_CJB110}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_COH1}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_M732}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_M781}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_18RS21}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_2603}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_A909}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_JM9130013}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_H36B}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
Consensus	*****	*****	*****	*****	*****

	901		930
msa521731.2{691_090}	TTTACAAA--	-----	-----
msa521731.2{691_1169NT}	TTTACAAA--	-----	-----
msa521731.2{691_CJB110}	TTTACAAA--	-----	-----
msa521731.2{691_COH1}	TTTACAAA--	-----	-----
msa521731.2{691_M732}	TTTACAAA--	-----	-----
msa521731.2{691_M781}	TTTACAAA--	-----	-----
msa521731.2{691_18RS21}	TTTACAAA--	-----	-----
msa521731.2{691_2603}	TTTACAAAgg	ctatcaaaga	aaatacaaat
msa521731.2{691_A909}	TTTACAAA--	-----	-----
msa521731.2{691_JM9130013}	TTTACAAA--	-----	-----
msa521731.2{691_H36B}	TTTACAAA--	-----	-----
Consensus	*****	*****	*****

SEQ ID NO. 8612

STRAIN 2603 frame: 1

MKKIGIIVLTLLTFFLVSCGQQTQESTKTTISKMPKIEGFTYYGKIPENPKKVINFTYS
 YTGILLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLTADDTEAIAAQKPDLMVFDQDPN
 INTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEANQWVSQWKTTLAVKKDLHHILK
 PNTTFTIMDFYDKNIYLYGNFGRGGELIYDSLGYAAPEKVKKDVFKKGWFTVSQEAIGD
 YVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHIIESNYDVFFYFSDPLSLEAQLKS
 FTKAIKENTN

SEQ ID NO. 8613

STRAIN 090 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGILLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN
 QWVSQWKTTLAAKDLHHILKPNNTTFTIMDFYDKNIYLYGNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8614

STRAIN A909 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGILLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN
 QWVSQWKTTLAAKDLHHILKPNNTTFTIMDFYDKNIYLYGNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8615

STRAIN H36B frame: 1

EGFTYYGKIPENPKKVINFTYSYTGILLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN
 QWVSQWKTTLAAKDLHHILKPNNTTFTIDFYDKNIYLYGNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8616

STRAIN 18RS21 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGILLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN
 QWVSQWKTTLAVKKDLHHILKPNNTTFTIMDFYDKNIYLYGNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8617

STRAIN M732 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGILLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN
 QWVSQWKTTLAAKDLHHILKPNNTTFTIMDFYDKNIYLYGNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8618

STRAIN COH1 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGILLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMPALGKVFGEKEAN

Table 86: Comparative Sequences relating to SAG1393

QWVSQWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8619

STRAIN M781 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLTA
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGKEKEAN
 QWVSQWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8620

STRAIN CJB110 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLTA
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGKEKEAN
 QWVSQWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8621

STRAIN 1169NT frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLTA
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGKEKEAN
 QWVSQWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8622

STRAIN JM9130013 frame: 1

EGFTYYGKIPENPKKVINFTYSYTGYYLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLTA
 DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMMPALGKVFGKEKEAN
 QWVSQWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNINKTTKKAASSLKESDVWKNLPAVKKGHI
 IESNYDVFFYFSDPLSLEAQLKSFT

PRETTY of: /biotmp/msa522124.2{*} April 28, 2003 08:17 ..

	1				50
msa522124.2{691_090}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_1169NT}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_CJB110}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_COH1}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_M732}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_M781}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_18RS21}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_2603}	mkkigiivlt	lltfflvscg	qqtqgestkt	tiskmpkieg	FTYYGKIPEN
msa522124.2{691_A909}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_JM9130013}	-----	-----	-----	-----	EG FTYYGKIPEN
msa522124.2{691_H36B}	-----	-----	-----	-----	EG FTYYGKIPEN
Consensus	*****	*****	*****	*****	*****
	51				100
msa522124.2{691_090}	PKKVINFTYS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLtADD
msa522124.2{691_1169NT}	PKKVINFTYS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLtADD
msa522124.2{691_CJB110}	PKKVINFTYS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLtADD
msa522124.2{691_COH1}	PKKVINFTYS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLtADD
msa522124.2{691_M732}	PKKVINFTYS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLtADD
msa522124.2{691_M781}	PKKVINFTYS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLtADD
msa522124.2{691_18RS21}	PKKVINFTYS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLtADD
msa522124.2{691_2603}	PKKVINFTYS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KeAKKLtADD
msa522124.2{691_A909}	PKKVINFTYS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KgAKKLtADD
msa522124.2{691_JM9130013}	PKKVINFTYS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KgAKKLtADD
msa522124.2{691_H36B}	PKKVINFTYS	YTGYYLLKLG	VNVSSYSLDLE	KDSPVFGKQL	KgAKKLtADD
Consensus	*****	*****	*****	*****	*-*****
	101				150
msa522124.2{691_090}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_1169NT}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_CJB110}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_COH1}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_M732}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_M781}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_18RS21}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_2603}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_A909}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
msa522124.2{691_JM9130013}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV

Table 86: Comparative Sequences relating to SAG1393

msa522124.2{691_H36B}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
Consensus	*****	*****	*****	*****	*****
	151				200
msa522124.2{691_090}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_1169NT}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_CJB110}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_COH1}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_M732}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_M781}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_18RS21}	FGKEKEANQW	VSQWKTKTTLA	vKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_2603}	FGKEKEANQW	VSQWKTKTTLA	vKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_A909}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_JM9130013}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_H36B}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
Consensus	*****	*****	*****	*****	*****
	201				250
msa522124.2{691_090}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_1169NT}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_CJB110}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_COH1}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_M732}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_M781}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_18RS21}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_2603}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_A909}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_JM9130013}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_H36B}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
Consensus	*****	*****	*****	*****	*****
	251				300
msa522124.2{691_090}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVIFYSD	PLSLEAQLKS
msa522124.2{691_1169NT}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVIFYSD	PLSLEAQLKS
msa522124.2{691_CJB110}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVIFYSD	PLSLEAQLKS
msa522124.2{691_COH1}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVIFYSD	PLSLEAQLKS
msa522124.2{691_M732}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVIFYSD	PLSLEAQLKS
msa522124.2{691_M781}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVIFYSD	PLSLEAQLKS
msa522124.2{691_18RS21}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVIFYSD	PLSLEAQLKS
msa522124.2{691_2603}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVIFYSD	PLSLEAQLKS
msa522124.2{691_A909}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVIFYSD	PLSLEAQLKS
msa522124.2{691_JM9130013}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVIFYSD	PLSLEAQLKS
msa522124.2{691_H36B}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIIE	SNYDVIFYSD	PLSLEAQLKS
Consensus	*****	*****	*****	*****	*****
	301	310			
msa522124.2{691_090}	FT-----				
msa522124.2{691_1169NT}	FT-----				
msa522124.2{691_CJB110}	FT-----				
msa522124.2{691_COH1}	FT-----				
msa522124.2{691_M732}	FT-----				
msa522124.2{691_M781}	FT-----				
msa522124.2{691_18RS21}	FT-----				
msa522124.2{691_2603}	FTkaikentn				
msa522124.2{691_A909}	FT-----				
msa522124.2{691_JM9130013}	FT-----				
msa522124.2{691_H36B}	FT-----				
Consensus	*****				

Table 87: Comparative Sequences relating to SAG0645

SEQ ID NO. 8701

STRAIN 2603

ATGAAATATCGAAGAAGTTATTGTTTTCGGCTGCTGTT
 TTAACAATGGTGGCGGGTCAACTGTTGAACCACTAGCTCAGTTTGGCGACTGGAATGAGT
 ATTGTAAGAGCTGCAGAAGTGTCAAGAAGCGCCAGCGAAAAACAACAGTAAATATCTAT
 AAATTACAAGCTGATAGTTATAAATCGGAAATTACTTCTAATGGTGGTATCGAGAATAAA
 GACGGCGAAGTAATATCTAACTATGCTAACTTGGTGACAATGTAAAAGGTTTGCAAGGT
 GTACAGTTTAAACGTTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTG
 ACAACAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTGAGTCTA
 CCTCAAAAACTAATGCTCAAGGTTTGGTCGTGATGCTCTGGATTCAAAAAAGTAATGTG
 AGATACTTGTATGTAGAAGATTTAAAGAATTACCTTCAAACATTACCAAAGCTTATGCT
 GTACCGTTTGTGTTGGAATTACCAGTTGCTAACTCTACAGGTACAGGTTTCCCTTCTGAA
 ATTAATATTTACCTTAAAAACGTTGTAACCTGATGAACCAAAACAGATAAAGATGTTAAA
 AAATTAGGTGAGGACGATGCAAGGTTATACGATTGGTGAAGAATTCAAATGGTTCTTGAAA
 TCTACAATCCCTGCCAATTAGGTGACTATGAAAAATTGAAATTAAGTATAAATTTGCA
 GATGGCTTGACTTATAAATCTGTTGGAATAAATCAAGATTGGTTGAAAAACACTGAATAGA
 GATGAGCACTACACTATTGATGAACCAACAGTTGATAACCAAAATACATTAATAATTACG
 TTTAAACAGAGAAATTTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCTTGTTTAAA
 AATCAAGATGCTCTTGTATAAAGCTACTGCAAAATACAGATGATGCGGCATTTTGGAAATT
 CCAAGTTGCTCAACTATTAATGAAAAAGCAGTTTAGGAAAGCAATTGAAAAATCTTTT
 GAAGTTCAATATGACATACTCTCTGATAAAGCTGACAAATCCAAACCACTAATCCTCCA
 AGAAACAGAGAGTTTCACTGTTGGGAAACGATTGTAAGAAAGACTCAACAGAAACA
 CAAACACTAGGTGGTCTGAGTTTGAATTTGTTGGCTTCTGATGGGACAGCAGTAAATGG
 ACAGATGCTCTTATTAAAGCGAATACTAATAAAAACTATATGCTGGAGAAGCTGTTACT
 GGGCAACCAATCAAAATTGAAATCAGATACAGACGGTACGTTTGAAGTTAAAGGTTTGGCT
 TATGCAAGTTGATGCGAATGCAAGGGTACAGCAGTAACCTTACAATTTAAAGAAACAAAA
 GCACCAGAAGGTTATGTAATCCCTGATAAAGAAATCGAGTTTACAGTATCAGAAACATCT
 TATAATACAAACCACTGACATCAGGTTGATAGTCTGATGCAACCTGATACAAATT
 AAAAAACAAACCACTGCTTCAATCCCTAATACTGGTGGTATGTTACGGCTATCTTTGTC
 GCTATCGGTGCTGCGGTGATGGCTTTTGTGTTAAGGGATGAAGCGTCTACAAAGAT
 AAC

SEQ ID NO. 8702

STRAIN 090

GCAGAAGTGTCAAGAAGCGCCAGCGAAAAAC
 AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
 CTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAATCTAT
 GCTAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACG
 TTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAA
 CAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTC
 AGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTGATGCTCTGGA
 TTTCAAAAAGTAAATGTGAGTACTTGTATGTAGAAGATTAAAGAATTAC
 CTTCAACATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCA
 GTTGCTAACTCTACAGGTACAGGTTTCTTTCTGAAATTAATATTTACCC
 TAAAAACGTTGTAACCTGATGAACCAAAACAGATAAAGATGTTAAAAAAT
 TAGGTGAGACGATGCAAGTTTATACGATTGGTGAAGAATTCAAATGGTTCT
 TTGAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTGAAAT
 TACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAATAATCA
 AGATTGGTTGCAAAACACTGAATAGAGATGAGCACTACACTATTGATGAA
 CCAACAGTTGATAACCAAAATACATTAATAAATACGTTTAAACAGAGAA
 ATTTAAAGAAATGCTGAGCTACTTAAAGGAATGACCTTGTAAAAAATC
 AAGATGCTCTTGATAAAGCTACTGCAAAATACAGATGATGCGGCATTTTGG
 GAAATTCAGTTGCACTCACTATTAAATGAAAAAGCAGTTTGGGAAAAAGC
 AATTGAAAAATCTTTTGAACCTCAATATGACCATACCTGATAAAGCTG
 ACAATCCAAACCATCTAATCTCCCAAGAAACAGAAAGTTCATACCTGGT
 GGGAAACGATTGTAAGAAAGACTCAACAGAAACACAAACACTAGGTGG
 TGCTGAGTTTGAATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAG
 ATGCTCTTATTAAGCGAATACTAATAAAAACTATATGCTGGAGAAGCT
 GTTACTGGGCAACCAATCAAATGAAATCACATACAGACGGTACGTTTGA
 GATTAAAGGTTTGGCTTATGCAAGTTGATGCGAATGCAAGGGTACAGCAG
 TAACTTACAAATTAAGAAACAAAGCACCAGAAGGTTATGTAATCCCT
 GATAAAGAAATCGAGTTTACAGTATCAGAAACATCTTATAATACAAACCC
 AACTGACATCAGGTTGATAGTGCTGATGCAACCTGATACAAATTAATA
 ACAACAAACGTCCTTCA

SEQ ID NO. 8703

STRAIN A909

GCAGAAGTGTCAAGAAGCGCCAGCGAA
 AACCAACAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAA
 TTACTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAAT
 TATGCTAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAA
 ACGTTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGA
 CAACAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGT
 GTCAAGCTTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTGATGCTCT
 GGAATCAAAAGTAAATGTGAGTACTTGTATGTAGAAGATTAAAGAATT
 CACCTTCAAAACATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTA
 CCAGTTGCTAACTCTACAGGTACAGGTTTCTTTCTGAAATTAATATTTA
 CCCTAAaAACGTTGTAACCTGATGAACCAAAACAGATAAAGATGTTAAAA
 AATTAGGTGAGGACGATGCAAGGTTATACGATTGGTGAAGAATTCAAATGG
 TTCTTGAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGA
 AATTACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGAAAAA
 TCAAGATTGGTTGAAAAACCTGAATAGAGATGAGCACTACACTATTGAT
 GAACCAACAGTTGATAACCAAAATACATTAATAATTACGTTTAAACAGAA

Table 87: Comparative Sequences relating to SAG0645

GAAATTTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCCTTGTAAAA
 ATCAAGATGCTCTTGATAAAGCTACTGCAATACAGATGATGCGGCATTT
 TTGGAAATTCAGTTGCAATCAACTATTAATGAAAAAGCAGTTTATAGGAAA
 AGCAATTGAAAACTCTTTGAACTTCAATATGACCATACTCCTGATAAAG
 CTGACAAATCCAAAACCATCTAATCCTCCAGAAAACCCAGAAAGTTCATACT
 GGTGGGAAACGATTTGTAAAGAAAGACTCAACAGAAACACAAACACTAGG
 TGGTGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGGA
 CAGATGCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAA
 GCTGTACTGGGCAACCAATCAAATGAAATCACAATCAGACGGTACGTT
 TGAGATTAAAGGTTTGGCTTATGCACTGATGCGAATGCAGAGGGTACAG
 CAGTAACCTTACAAATTAAAAAGAAAACAAAGCACCAGAGGTTATGTAATC
 CCTGATAAAGAAATCGAGTTTACAGTATCACAACATCTTATAATACAAA
 ACCAACTGACATCACGGTTGATAGTCTGATGCAACACCTGATACAAATTA
 AAAACAACAA

SEQ ID NO. 8704

STRAIN 18RS21

GCAGAAGTGTCAAGAAGCGCCAGCGAAAAAC
 AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
 CTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTAT
 GCTAAACTTGGTGACAATGTAAAAGGTTTGCAAGGTGTACAGTTTAAACG
 TTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAA
 CAGTTGAAGCAGCAGATGCAAAAGTTGGAAACGATCTTGAAGAAGGTGTC
 AGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTGATGCTCTGGA
 TTCAAAAGTAATGTGAGATACTTGTATGTAGAAGATTAAAGAATTACAC
 CTTCAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCA
 GTTGCTAACTCTACAGGTACAGGTTTCCCTTCTGAAATTAATATTTACCC
 TAAAAACGTTGTAACCTGATGAACCAAAAAAGATGTTAAATAAT
 TAGGTACAGACGATGCAAGGTTATACGATTGGTGAAGAATTCAAATGGTTC
 TTGAAATCTACAATCCCTGCCAATTAGGTGACTATGAAAAATTTGAAAT
 TACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGAAAAATCA
 AGATTGGTTGCAAAACACTGAATAGAGATGAGCACTACACTATTGATGAA
 CCACAGTTGATAACCAAAATACATTAAAAAATTACGTTTAAACCAAGAGAA
 ATTTAAAGAAATTTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAAATC
 AAGATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTTTGTG
 GAAATTCAGTTGCATCAACTATTAAATGAAAAAGCAGTTTATAGGAAAAGC
 AATTGAAAAATCTTTTGAACCTCAATATGACCACTACTCCTGATAAAGCTG
 ACAATCCAAACCATCTAATCCTCCAGAAAACCCAGAAAGTTCATACTGGT
 GGGAAACGATTTGTAAAGAAAGACTCAACAGAAAACACAAACCTAGGTGG
 TGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAG
 ATGCTCTTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCT
 GTTACTGGGCAACCAATCAAATTTGAAATCACAATCAGACGGTACGTTTGA
 GATTAAAGGTTTGGCTTATGCACTGATGCGAATGCAGAGGGTACAGCAG
 TAACCTTACAAATTTAAAGAAACAAAGCACCAGAGGTTATGTAATCCCT
 GATAAAGAAATCGAGTTTACAGTATCACAACATCTTATAATACAAAAC
 AACTGACATCACGGTTGATAGTCTGATGCAACACCTGATACAAATTA
 ACAACAAACGTCCTTCA

SEQ ID NO. 8705

STRAIN M732

GCAGAAGTGTCAAGAAGCGCCAGCGAAAAACAGT
 AAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTAATCTTA
 ATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGCTAAA
 CTTGGTGACAATGTAAAGGTTTGCAAGGTGTACAGTTTAAACGTTATAA
 AGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACAGTGTG
 AAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTGAGTCTA
 CCTCAAAAACTAATGCTCAAGGTTTGGTCGTGATGCTCTGGATTCAAA
 AAGTAATGTGAGATACTTGTATGTAGAAGATTAAAGAATTACCTTCAA
 ACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACAGTTGCT
 AACTCTACAGGTACAGGTTTCTTTCTGAAATTAATATTACCCTAAAAA
 CGTTGTAACTGATGAACCAAAACAGATAAAGATGTTAAAAAATTAGGTC
 AGGACGATGCAAGTTATACGATTGGTGAAGAAATCAAATGGTTCTTGAAA
 TCTACAATCCCTGCCAATTTAGGTGACTATGAAAAAATTGAAATTACTGA
 TAAATTTGAGATGGCTTGACTTATAAATCTGTTGAAAAAATCAAGATTG
 GTTCGAAAACTGAATAGAGATGAGCACTACACTATTGATGAACCAACA
 GTTGATAACCAAAATACATTAAAAATTACGTTTAAACCAAGAGAAATTTAA
 AGAAATTTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAAATCAAGATG
 CTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTTTGGAAATT
 CCAGTTGCATCAACTATTAATGAAAAAGCAGTTTATAGGAAAAGCAATTGA
 AAATACTTTTGAACCTCAATATGACCATACTCCTGATAAAGCTGACAATC
 CAAAACCATCTAATCCTCCAGAAAACCCAGAAAGTTCATACTGGTGGGAAA
 CGATTGTAAAGAAAGACTCAACAGAAAACACAAACACTAGGTGGTGTGA
 GTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAGATGCTC
 TTATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGTTACT
 GGGCAACCAATCAAATTTGAAATCACAATCAGACGGTACGTTTGAATTA
 AGGTTTGGCTTATGCACTTGTGCGAATGCAGAGGGTACAGCAGTAACCT
 ACAATTTAAAGAAACAAAGCACCAGAGGTTATGTAATCCCTGATAAA
 GAAATCGAGTTTACAGTATCACAACATCTTATAATACAAAACCACTGA
 CATCACGGTTGATAGTCTGATGCAACACCTGATACAAATTAACCAACA
 AACGTCCTTCA

SEQ ID NO. 8706

STRAIN COH1

Table 87: Comparative Sequences relating to SAG0645

GCAGAAGTGTCAACAAGACGCCAGCGAAAAC
 AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
 CTTnTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTAT
 GCTAAACTTGGTGACAATGTAAAGGTTTGCAGGTGTACAGTTTAAACG
 TTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAA
 CAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTC
 AGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGA
 TTCAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTCAC
 CTTCAAAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCA
 GTTGCTAACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATTACCC
 TAAAAACGTTGTAACGTGATGAACCAAAACAGATAAAGATGTTAAAAAAT
 TAGGTGAGGACGATGACAGTTTATACGATTGGTGAAGAATTCAAATGGTTC
 TTGAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAAATTGAAAT
 TACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAATAATCA
 AGATTGGTTGCAAAACACTGAATAGAGATGAGCACTACACTATTGATGAA
 CCAACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACAGAGAA
 ATTTAAAGAAATGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAAATC
 AAGATGCTCTTGATAAAGCTACTGCAATACAGATGATGCGGCATTTTGTG
 GAAATTCAGTTGCATCAACTATTAAATGAAAAAGCAGTTTTAGGAAAAAGC
 AATTGAAAAATACTTTGAACCTTCAATATGACCATACTCCTGATAAAGCTG
 ACAATCCAAACCAATCTAATCCTCCAAGAAACAGAAAGTTCACTAGGT
 GGGAAACGATTTGTAAGAAAGACTCAACAGAAACACAAACACTAGGTGG
 TGCAGGTTTGTGTTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAG
 ATGCTCTTATAAAGCGAATACTAATAAAAACTATATTGCTGGAGAGCT
 GTTACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGA
 GATTAAGGTTTGGCTTATGCAAGTTGATGCGAATGACAGGGGTACAGCAG
 TAACTTCAAAATTAAGAAACAAAGCACCAGAGGTTATGTAATCCCT
 GATAAAGAAATCGAGTTTACAGTATCAAAACATCTTATAATACAAACCC
 AACTGACATACCGTTGATAGTGTGATGCAACACCTGATACAATTAATA
 ACAACAAACGTCCTTCA

SEQ ID NO. 8707

STRAIN M781

GCAGAAGTGTCAACAAGACGCCAGCGAAAACAG
 CAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
 TCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGC
 TAAACTTGGTGACAATGTAAAGGTTTGCAGGTGTACAGTTTAAACGTT
 ATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACA
 GTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTGAG
 TCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCTGGATT
 CAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTACCT
 TCAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACAGT
 TGCTAACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATTACCTTA
 AAAACGTTGTAACTGATGAACCAAAACAGATAAAGATGTTAAAAAATTA
 GGTGAGGACGATGACAGTTTATACGATTGGTGAAGAATTCAAATGGTTCTT
 GAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTGAAATTA
 CTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAATAATCAAG
 ATTGGTTGCAAAACACTGAATAGAGATGAGCACTACACTATTGATGAACC
 AACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACAGAGAAAT
 TTAAGAAATTTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAAATCAA
 GATGCTCTTGATAAGCTACTGCAAAATACAGATGATGCGGCATTTTGGTA
 AATTCCAGTTGCATCAACTATTAAATGAAAAAGCAGTTTTAGGAAAAAGCAA
 TTGAAAAATCTTTTGAACCTTCAATATGACCATACTCCTGATAAAGCTGAC
 AATCCAAACCAATCTAATCCTCCAAGAAACAGAAAGTTCACTAGGTGG
 GAAACGATTTGTAAGAAAGACTCAACAGAAACACAAACACTAGGTGGTG
 CTGAGTTTGTGTTTGGCTTCTGATGGGACAGCAGTAAATGGACAGAT
 GCTCTTATTAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGT
 TACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGA
 TTAAGGTTTGGCTTATGCAAGTTGATGCGAATGACAGGGGTACAGCAGTA
 ACTTACAAATTAAGAAACAAAGCACCAGAAAGTTATGTAATCCCTGA
 TAAAGAAATCGAGTTTACAGTATCAAAACATCTTATAATACAAACCAA
 CTGACATACCGTTGATAGTGTGATGCAACACCTGATACAATTAATAAC
 AACAAACGT

SEQ ID NO. 8708

STRAIN CJB110

GCAGAAGTGTCAACAAGACGCCAGCGAA
 AACAGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATGGAAA
 TTACTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAAC
 TATGCTAAACTTGGTGACAATGTAAAGGTTTGCAGGTGTACAGTTTAA
 ACGTTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGA
 CAACAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGT
 GTGAGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATGCTCT
 GGATTCAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATT
 CACCTTCAAAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTA
 CCAAGTTGCTAACTCTACAGGTACAGGTTTCCTTTCTGAAATTAATATT
 CCTTAAAAACGTTGTAATGATGAACCAAAACAGATAAAGATGTTAAAA
 AATTAGGTGAGGACGATGACAGTTTATACGATTGGTGAAGAATTCAAATGG
 TTCTTGAAGTCTACAATCCCTGCCAATTTAGGTGACTATGAAAAAATTGA
 AATTACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAATA
 TCAAGATTGGTTGAAAAACACTGAATAGAGATGAGCACTACACTATTGAT
 GAACCAACAGTTGATAACCAAAATACATTAAAAATTACGTTTAAACAGAA
 GAAATTTAAAGAAATTTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAA

Table 87: Comparative Sequences relating to SAG0645

ATCAAGATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATT
 TTGGAAATTCAGTTGTCATCAACTATTAATGAAAAAGCAGTTTATAGGAA
 AGCAATTGAAAACTCTTTGAACTTCAATATGACCATACTCTGATAAAG
 CTGCAATcCAAAACCATCTAATCTCCAGAAAACAGAGTTCTACT
 GGTGGGAAACGATTTGTAAAGAAAGACTCAACAGAAAACAAACACTAGG
 TGGTGCTGAGTTTGATTGTTGGCTTCTGATGGGACAGCAGTAAATGGA
 CAGATGCTCTTATTAAGCGAATACTAATAAAAACTATATTGCTGGAGAA
 GCTGTTACTGGGCAACCAATCAAAATGAAATCAGATACAGACGGTACGTT
 TGAGATTAAAGGTTTGGCTTATGCGAGTTGATGCGAATGCAGAGGGTACAG
 CAGTAACCTACAAATTAAAGAAAACAAAGCACCAGAGGTTATGTAATC
 CCTGATAAAGAAATCGAGTTTACAGTATCAGAAACATCTTATAATCCAA
 ACCAATGACATCAGGTTGATAGTCTGATGCAACACCTGATACAATTA
 AAAACAACAAACGCTCCTCA

SEQ ID NO. 8709

STRAIN JM9130013

GCAGAAGTGTCAAGAACGCCAGCGAAAACAGCAGTA
 AATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACTTCTAA
 TGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGCTAAAC
 TTGGTGACAAATGTAAGGTTTGAAGGTGATCAGTTTAAACGTTATAAA
 GTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACAGTTGA
 AGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTCAGTCTAC
 CTCAAAAAATAATGCTCAAGGTTTGGTCTGTCGATGCTCTGGATTCAAAA
 AGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTACCTTCAAA
 CATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACAGTTGCTA
 ACTCTACAGGTACAGGTTTCCCTTCTGAAATTAATATTACCTTAAAAAC
 GTTGTAACTGATGAACCAAAAACAGATAAAGATGTTAAAAAATTAGGTCA
 GGACGATGCGAGTTATACGATTGGTGAAGAATTCAAAATGGTTCTTGAAAT
 CTACAATCCCTGCCAATTTAGGTGACTATGAAAAAATTGAAATTACTGAT
 AAATTTGAGATGGCTTGACTTATAAATCTGTTGGAATAACAGATTGG
 TTCGAAAACACTGAATAGAGATGAGCACTACACTATTGATGAACCAACAG
 TTGATAACCAAAATACATTAAAAATTACGTTTAAACAGAGAAATTTAAA
 GAAATTTGCTGAGCTACTTAAAGGAATGACCTTGTATAAAATCAAGATGC
 TCTTGATAAAGCTACTGCAAAATACAGATGATGCGGCATTTTGGAAATTC
 CAGTTGCTCAACTATTAAATGAAAAGCAGTTTATAGGAAAAGCAATTGAA
 AATACTTTTGAACCTTCAATATGACCATACTCTGATAAAGCTGACAAATCC
 AAAACCATCTAATcCTcCAAGAAAACAGAAAGTTCATCTGTTGGGAAAC
 GATTGTGTAAGAAAGACTCAACAGAAAACAAACACTAGGTGGTGTCTGAG
 TTTGATTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAGATGCTCT
 TATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGTTACTG
 GGCACCAATCAAATTGAAATCAGATACAGACGGTACGTTTGGATTAA
 GGTTTGGCTTATGCAATTGATGCGAATGCAGAGGGTACAGCAGTAACCTA
 CAAATTAAGAAAACAAAGCACCAGAGGTTATGTAATCCCTGATAAAG
 AATCGAGTTTACAGTATCAGAAACATCTTATAATCAAAAACCACTGAC
 ATCAGGTTGATAGTCTGATGCAACACCTGATACAATTA AAAACAACAA
 ACGTCTCTCA

PRETTY of: /biotmp/msa123961.2{*} April 30, 2003 07:17 ..

	1				50
msa123961.2{80_2603}	atgaaattat	cgaagaagtt	attgtttttcg	gctgctgttt	taacaatggt
msa123961.2{80_A909}	-----	-----	-----	-----	-----
msa123961.2{80_M732}	-----	-----	-----	-----	-----
msa123961.2{80_090}	-----	-----	-----	-----	-----
msa123961.2{80_COH1}	-----	-----	-----	-----	-----
msa123961.2{80_M781}	-----	-----	-----	-----	-----
msa123961.2{801_JM9130013}	-----	-----	-----	-----	-----
msa123961.2{80_18RS21}	-----	-----	-----	-----	-----
msa123961.2{80h_CJB110}	-----	-----	-----	-----	-----
Consensus	-----	-----	-----	-----	-----

	51				100
msa123961.2{80_2603}	ggcgggggtca	actgttgaac	cagtagctca	gtttgcgact	ggaatgagta
msa123961.2{80_A909}	-----	-----	-----	-----	-----
msa123961.2{80_M732}	-----	-----	-----	-----	-----
msa123961.2{80_090}	-----	-----	-----	-----	-----
msa123961.2{80_COH1}	-----	-----	-----	-----	-----
msa123961.2{80_M781}	-----	-----	-----	-----	-----
msa123961.2{801_JM9130013}	-----	-----	-----	-----	-----
msa123961.2{80_18RS21}	-----	-----	-----	-----	-----
msa123961.2{80h_CJB110}	-----	-----	-----	-----	-----
Consensus	-----	-----	-----	-----	-----

	101				150
msa123961.2{80_2603}	ttgtaagagc	tGCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_A909}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_M732}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_090}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_COH1}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_M781}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{801_JM9130013}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA
msa123961.2{80_18RS21}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAaCAGTA

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80h_CJB110}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAgCAGTA
Consensus	-----	*****	*****	*****	*****
msa123961.2{80_2603}	151	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA
msa123961.2{80_A909}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA
msa123961.2{80_M732}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA
msa123961.2{80_090}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA
msa123961.2{80_COH1}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA
msa123961.2{80_M781}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA
msa123961.2{801_JM9130013}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA
msa123961.2{80_18RS21}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA
msa123961.2{80h_CJB110}		AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA
Consensus		*****	*****	*****	*****
msa123961.2{80_2603}	201	TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC
msa123961.2{80_A909}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC
msa123961.2{80_M732}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC
msa123961.2{80_090}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC
msa123961.2{80_COH1}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC
msa123961.2{80_M781}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC
msa123961.2{801_JM9130013}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC
msa123961.2{80_18RS21}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC
msa123961.2{80h_CJB110}		TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC
Consensus		*****	*****	*****	*****
msa123961.2{80_2603}	251	TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA
msa123961.2{80_A909}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA
msa123961.2{80_M732}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA
msa123961.2{80_090}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA
msa123961.2{80_COH1}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA
msa123961.2{80_M781}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA
msa123961.2{801_JM9130013}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA
msa123961.2{80_18RS21}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA
msa123961.2{80h_CJB110}		TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTTAA
Consensus		*****	*****	*****	*****
msa123961.2{80_2603}	301	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA
msa123961.2{80_A909}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA
msa123961.2{80_M732}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA
msa123961.2{80_090}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA
msa123961.2{80_COH1}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA
msa123961.2{80_M781}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA
msa123961.2{801_JM9130013}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA
msa123961.2{80_18RS21}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA
msa123961.2{80h_CJB110}		GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA
Consensus		*****	*****	*****	*****
msa123961.2{80_2603}	351	AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT
msa123961.2{80_A909}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT
msa123961.2{80_M732}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT
msa123961.2{80_090}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT
msa123961.2{80_COH1}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT
msa123961.2{80_M781}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT
msa123961.2{801_JM9130013}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT
msa123961.2{80_18RS21}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT
msa123961.2{80h_CJB110}		AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT
Consensus		*****	*****	*****	*****
msa123961.2{80_2603}	401	CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT
msa123961.2{80_A909}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT
msa123961.2{80_M732}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT
msa123961.2{80_090}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT
msa123961.2{80_COH1}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT
msa123961.2{80_M781}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT
msa123961.2{801_JM9130013}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT
msa123961.2{80_18RS21}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT
msa123961.2{80h_CJB110}		CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT
Consensus		*****	*****	*****	*****
msa123961.2{80_2603}	451	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT
msa123961.2{80_A909}		AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT
msa123961.2{80_M732}		AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT
msa123961.2{80_090}		AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT
msa123961.2{80_COH1}		AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT
msa123961.2{80_M781}		AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT
msa123961.2{801_JM9130013}		AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80_18RS21}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA
msa123961.2{80h_CJB110}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA
Consensus	*****	*****	*****	*****	*****
501					
msa123961.2{80_2603}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_A909}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_M732}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_090}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_COH1}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_M781}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{801_JM9130013}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_18RS21}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80h_CJB110}	CATTACCAAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
Consensus	*****	*****	*****	*****	*****
551					
msa123961.2{80_2603}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_A909}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_M732}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_090}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_COH1}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_M781}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{801_JM9130013}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_18RS21}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80h_CJB110}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
Consensus	*****	*****	*****	*****	*****
601					
msa123961.2{80_2603}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAa	AATTAGGTCA
msa123961.2{80_A909}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAa	AATTAGGTCA
msa123961.2{80_M732}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAa	AATTAGGTCA
msa123961.2{80_090}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAa	AATTAGGTCA
msa123961.2{80_COH1}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAa	AATTAGGTCA
msa123961.2{80_M781}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAa	AATTAGGTCA
msa123961.2{801_JM9130013}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAa	AATTAGGTCA
msa123961.2{80_18RS21}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAa	AATTAGGTCA
msa123961.2{80h_CJB110}	GTGTAACTG	ATGAACCAAA	AACAGATAAA	GATGTTAAa	AATTAGGTCA
Consensus	*****	*****	*****	*****	*****
651					
msa123961.2{80_2603}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_A909}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_M732}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_090}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_COH1}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_M781}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{801_JM9130013}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80_18RS21}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
msa123961.2{80h_CJB110}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAAT
Consensus	*****	*****	*****	*****	*****
701					
msa123961.2{80_2603}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_A909}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_M732}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_090}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_COH1}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_M781}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{801_JM9130013}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_18RS21}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80h_CJB110}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
Consensus	*****	*****	*****	*****	*****
751					
msa123961.2{80_2603}	AAATTTCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_A909}	AAATTTCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_M732}	AAATTTCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_090}	AAATTTCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_COH1}	AAATTTCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_M781}	AAATTTCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{801_JM9130013}	AAATTTCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_18RS21}	AAATTTCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80h_CJB110}	AAATTTCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
Consensus	*****	*****	*****	*****	*****
801					
msa123961.2{80_2603}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTGAT	GAACCAACAG
msa123961.2{80_A909}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTGAT	GAACCAACAG
msa123961.2{80_M732}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTGAT	GAACCAACAG
msa123961.2{80_090}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTGAT	GAACCAACAG
msa123961.2{80_COH1}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTGAT	GAACCAACAG
msa123961.2{80_M781}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTGAT	GAACCAACAG

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{801_JM9130013}	TTCGAAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
msa123961.2{80_18RS21}	TTCGAAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
msa123961.2{80h_CJB110}	TTCGAAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
Consensus	*****	*****	*****	*****	*****
	851				900
msa123961.2{80_2603}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_A909}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_M732}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_090}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_COH1}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_M781}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{801_JM9130013}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_18RS21}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80h_CJB110}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
Consensus	*****	*****	*****	*****	*****
	901				950
msa123961.2{80_2603}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{80_A909}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{80_M732}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{80_090}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{80_COH1}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{80_M781}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{801_JM9130013}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{80_18RS21}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{80h_CJB110}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
Consensus	*****	*****	*****	*****	*****
	951				1000
msa123961.2{80_2603}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_A909}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_M732}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_090}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_COH1}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_M781}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{801_JM9130013}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_18RS21}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80h_CJB110}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
Consensus	*****	*****	*****	*****	*****
	1001				1050
msa123961.2{80_2603}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{80_A909}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{80_M732}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{80_090}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{80_COH1}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{80_M781}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{801_JM9130013}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{80_18RS21}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
msa123961.2{80h_CJB110}	CAGTTGCATC	AACATTAAAT	GAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA
Consensus	*****	*****	*****	*****	*****
	1051				1100
msa123961.2{80_2603}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_A909}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_M732}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_090}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_COH1}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_M781}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{801_JM9130013}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_18RS21}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80h_CJB110}	AATACITTTG	AACITCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
Consensus	*****	*****	*****	*****	*****
	1101				1150
msa123961.2{80_2603}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_A909}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_M732}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_090}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_COH1}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_M781}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{801_JM9130013}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_18RS21}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80h_CJB110}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
Consensus	*****	*****	*****	*****	*****
	1151				1200
msa123961.2{80_2603}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{80_A909}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{80_M732}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{80_090}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{80_COH1}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80_M781}	GATTGTGAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCCTGAG
msa123961.2{801_JM9130013}	GATTGTGAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCCTGAG
msa123961.2{80_18RS21}	GATTGTGAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCCTGAG
msa123961.2{80h_CJB110}	GATTGTGAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCCTGAG
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_A909}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_M732}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_090}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_COH1}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_M781}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{801_JM9130013}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80_18RS21}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
msa123961.2{80h_CJB110}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAAAATGGA	CAGATGCTCT
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_A909}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_M732}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_090}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_COH1}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_M781}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{801_JM9130013}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_18RS21}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80h_CJB110}	TATTAAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_A909}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_M732}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_090}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_COH1}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_M781}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{801_JM9130013}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_18RS21}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80h_CJB110}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_A909}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_M732}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_090}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_COH1}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_M781}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{801_JM9130013}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_18RS21}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80h_CJB110}	GGTTTGGCTT	ATGCAGTTGA	TGCGAATGCA	GAGGGTACAG	CAGTAACCTA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	CAAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_A909}	CAAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_M732}	CAAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_090}	CAAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_COH1}	CAAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_M781}	CAAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{801_JM9130013}	CAAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_18RS21}	CAAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80h_CJB110}	CAAAATTAAAA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_A909}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_M732}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_090}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_COH1}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_M781}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{801_JM9130013}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_18RS21}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80h_CJB110}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_A909}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_M732}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_090}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80_COH1}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_M781}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{801_JM9130013}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_18RS21}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80h_CJB110}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	acgtccttca	atccctaata	ctgggtggtat	tggtacggct	atctttgtcg
msa123961.2{80_A909}	-----	-----	-----	-----	-----
msa123961.2{80_M732}	acgtccttca	-----	-----	-----	-----
msa123961.2{80_090}	acgtccttca	-----	-----	-----	-----
msa123961.2{80_COH1}	acgtccttca	-----	-----	-----	-----
msa123961.2{80_M781}	acgt-----	-----	-----	-----	-----
msa123961.2{801_JM9130013}	acgtccttca	-----	-----	-----	-----
msa123961.2{80_18RS21}	acgtccttca	-----	-----	-----	-----
msa123961.2{80h_CJB110}	acgtccttca	-----	-----	-----	-----
Consensus	-----	-----	-----	-----	-----
msa123961.2{80_2603}	ctatcgggtgc	tgccggtgatg	gctttttgctg	ttaaggggat	gaagcgtcgt
msa123961.2{80_A909}	-----	-----	-----	-----	-----
msa123961.2{80_M732}	-----	-----	-----	-----	-----
msa123961.2{80_090}	-----	-----	-----	-----	-----
msa123961.2{80_COH1}	-----	-----	-----	-----	-----
msa123961.2{80_M781}	-----	-----	-----	-----	-----
msa123961.2{801_JM9130013}	-----	-----	-----	-----	-----
msa123961.2{80_18RS21}	-----	-----	-----	-----	-----
msa123961.2{80h_CJB110}	-----	-----	-----	-----	-----
Consensus	-----	-----	-----	-----	-----
msa123961.2{80_2603}	acaaaagata	ac			
msa123961.2{80_A909}	-----	--			
msa123961.2{80_M732}	-----	--			
msa123961.2{80_090}	-----	--			
msa123961.2{80_COH1}	-----	--			
msa123961.2{80_M781}	-----	--			
msa123961.2{801_JM9130013}	-----	--			
msa123961.2{80_18RS21}	-----	--			
msa123961.2{80h_CJB110}	-----	--			
Consensus	-----	--			

SEQ ID NO. 8710

STRAIN 2603 frame: 1

MKLSKKLLFSAAVLTVMAGSTVEPVAQFATGMSIVRAAEVSQERPAKTTVNIYKLQADSY
 KSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFKRYKVKTDISVDELKKLTTVEAAD
 AKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLYVEDLKNSPSNITKAYAVPFVLEL
 PVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQDDAGYTI GEEFKWFLKSTIPANL
 GDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHYTIDEPTVDNONTLKITFKPEKFK
 EIAELLKGMTLVKNQDALDKATANTDDAAFLAIPVASTINEKAVLGKAIENTFELQYDHT
 PDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLGGAEFDLLASDGTAVKWTDALIKA
 NTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVDANAEGTAVTYKLKETKAPEGYVI
 PDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNKRPSIPTGTGIGTAIFVAIGAAMV
 AFAVKGMRRTKDN

SEQ ID NO. 8711

STRAIN 090 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
 VEDLKNSPSNITKAYAVPFVLEL PVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
 DDAGYTI GEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNONTLKITFKPEKFK EIAELLKGMTLVKNQDALDKATANTDDAAFLAIPVAS
 TINEKAVLGKAIENTFELQYDHTPKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQ ID NO. 8712

STRAIN 18RS21 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK
 RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
 VEDLKNSPSNITKAYAVPFVLEL PVANSTGTGFLSEINIYPKNVVTDEPKTDKDVK.LGQ
 DDAGYTI GEEFKWFLKSTIPANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNONTLKITFKPEKFK EIAELLKGMTLVKNQDALDKATANTDDAAFLAIPVAS
 TINEKAVLGKAIENTFELQYDHTPKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQ ID NO. 8713

STRAIN M732 frame: 1

AEVSQERPAKTTVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFK

Table 87: Comparative Sequences relating to SAG0645

RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYEFKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLAIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANABGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8714

STRAIN M781 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVINSYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYEFKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLAIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANABGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
R

SEQ ID NO. 8715

STRAIN COH1 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVINSYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYEFKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLAIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANABGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8716

STRAIN CJB110 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVINSYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYEFKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLAIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANABGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8717

STRAIN JM9130013 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVINSYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYEFKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLAIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANABGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8718

STRAIN A909 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVINSYAKLGDNVKGLQGVQFK
RYKVKTDISVDELKLLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTIIEEFKWLKSTIPANLGDYEFKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKIITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLAIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIKLKSHTDGTFEIKGLAYAVD
ANABGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK

PRETTY of: /biotmp/msa124060.2{*} April 30, 2003 07:19 ..

	1		50
msa124060.2{80_2603}	mklskklfs aavltmvags tvepvafat gmsivraAEV	SQERPAKtTv	
msa124060.2{80_M732}	-----	AEV	SQERPAKtTv
msa124060.2{80_A909}	-----	AEV	SQERPAKtTv
msa124060.2{80_090}	-----	AEV	SQERPAKtTv
msa124060.2{80_M781}	-----	AEV	SQERPAKtTv
msa124060.2{80_COH1}	-----	AEV	SQERPAKtTv
msa124060.2{801_JM9130013}	-----	AEV	SQERPAKtTv
msa124060.2{80_18RS21}	-----	AEV	SQERPAKtTv
msa124060.2{80h_CJB110}	-----	AEV	SQERPAKtTv
Consensus	-----	***	*****

Table 87: Comparative Sequences relating to SAG0645

	51		100
msa124060.2{80_2603}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{80_M732}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{80_A909}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{80_090}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{80_M781}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{80_COH1}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{801_JM9130013}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{80_18RS21}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
msa124060.2{80h_CJB110}	NIYKLQADSY KsEITsNGGI ENKDGIVSN YAKLGDNVKG LQGVQFKRYK		
Consensus	***** *--*--*--* ***** ***** *****		
	101		150
msa124060.2{80_2603}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{80_M732}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{80_A909}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{80_090}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{80_M781}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{80_COH1}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{801_JM9130013}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{80_18RS21}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
msa124060.2{80h_CJB110}	VKTDISVDEL KKLTTVEAAD AKVGTILEEG VSLPQKTNAQ GLVVDALDSK		
Consensus	***** ***** ***** ***** *****		
	151		200
msa124060.2{80_2603}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{80_M732}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{80_A909}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{80_090}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{80_M781}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{80_COH1}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{801_JM9130013}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{80_18RS21}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
msa124060.2{80h_CJB110}	SNVRYLYVED LKNSPSNITK AYAVPFVLEL PVANSTGTGF LSEINIYPKN		
Consensus	***** ***** ***** ***** *****		
	201		250
msa124060.2{80_2603}	VVTDEPKTDK DVKKLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{80_M732}	VVTDEPKTDK DVKKLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{80_A909}	VVTDEPKTDK DVKKLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{80_090}	VVTDEPKTDK DVKKLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{80_M781}	VVTDEPKTDK DVKKLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{80_COH1}	VVTDEPKTDK DVKKLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{801_JM9130013}	VVTDEPKTDK DVKKLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{80_18RS21}	VVTDEPKTDK DVK.LGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
msa124060.2{80h_CJB110}	VVTDEPKTDK DVKKLGQDDA GYTIGEEFKW FLKSTIPANL GDYEKFEITD		
Consensus	***** ***-***** ***** ***** *****		
	251		300
msa124060.2{80_2603}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{80_M732}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{80_A909}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{80_090}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{80_M781}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{80_COH1}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{801_JM9130013}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{80_18RS21}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
msa124060.2{80h_CJB110}	KFADGLTYKS VGKIKIGSKT LNRDEHYTID EPTVDNQNTL KITFKPEKFK		
Consensus	***** ***** ***** ***** *****		
	301		350
msa124060.2{80_2603}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{80_M732}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{80_A909}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{80_090}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{80_M781}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{80_COH1}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{801_JM9130013}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{80_18RS21}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
msa124060.2{80h_CJB110}	EIAELLKGMT LVKNQDALDK ATANTDDAAF LEIPVASTIN EKAVLGKAIE		
Consensus	***** ***** ***** ***** *****		
	351		400
msa124060.2{80_2603}	NTFELQYDHT PDKADNPKPS NPPRKPEVHT GKKRFVKKDS TETQTLGGAE		
msa124060.2{80_M732}	NTFELQYDHT PDKADNPKPS NPPRKPEVHT GKKRFVKKDS TETQTLGGAE		
msa124060.2{80_A909}	NTFELQYDHT PDKADNPKPS NPPRKPEVHT GKKRFVKKDS TETQTLGGAE		
msa124060.2{80_090}	NTFELQYDHT PDKADNPKPS NPPRKPEVHT GKKRFVKKDS TETQTLGGAE		
msa124060.2{80_M781}	NTFELQYDHT PDKADNPKPS NPPRKPEVHT GKKRFVKKDS TETQTLGGAE		
msa124060.2{80_COH1}	NTFELQYDHT PDKADNPKPS NPPRKPEVHT GKKRFVKKDS TETQTLGGAE		
msa124060.2{801_JM9130013}	NTFELQYDHT PDKADNPKPS NPPRKPEVHT GKKRFVKKDS TETQTLGGAE		
msa124060.2{80_18RS21}	NTFELQYDHT PDKADNPKPS NPPRKPEVHT GKKRFVKKDS TETQTLGGAE		
msa124060.2{80h_CJB110}	NTFELQYDHT PDKADNPKPS NPPRKPEVHT GKKRFVKKDS TETQTLGGAE		
Consensus	***** ***** ***** ***** *****		

Table 87: Comparative Sequences relating to SAG0645

	401			450
msa124060.2{80_2603}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{80_M732}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{80_A909}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{80_090}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{80_M781}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{80_COH1}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{801_JM9130013}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{80_18RS21}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
msa124060.2{80h_CJB110}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLLK SHTDGTFEIK
Consensus	*****	*****	*****	*****
	451			500
msa124060.2{80_2603}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{80_M732}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{80_A909}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{80_090}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{80_M781}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{80_COH1}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{801_JM9130013}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{80_18RS21}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNtKPTD
msa124060.2{80h_CJB110}	GLAYAVDANA	EGTAVTYKLLK	ETKAPEGYVI	PDKEIEFTVS QTSYNpKPTD
Consensus	*****	*****	*****	*****
	501			550
msa124060.2{80_2603}	ITVDSADATP	DTIKNNkrps	ipntggigta	ifvaigaavm afavkgmkrr
msa124060.2{80_M732}	ITVDSADATP	DTIKNNkrps	-----	-----
msa124060.2{80_A909}	ITVDSADATP	DTIKNN----	-----	-----
msa124060.2{80_090}	ITVDSADATP	DTIKNNkrps	-----	-----
msa124060.2{80_M781}	ITVDSADATP	DTIKNNkr--	-----	-----
msa124060.2{80_COH1}	ITVDSADATP	DTIKNNkrps	-----	-----
msa124060.2{801_JM9130013}	ITVDSADATP	DTIKNNkrps	-----	-----
msa124060.2{80_18RS21}	ITVDSADATP	DTIKNNkrps	-----	-----
msa124060.2{80h_CJB110}	ITVDSADATP	DTIKNNkrps	-----	-----
Consensus	*****	*****	-----	-----
	551			
msa124060.2{80_2603}	tkdn			
msa124060.2{80_M732}	----			
msa124060.2{80_A909}	----			
msa124060.2{80_090}	----			
msa124060.2{80_M781}	----			
msa124060.2{80_COH1}	----			
msa124060.2{801_JM9130013}	----			
msa124060.2{80_18RS21}	----			
msa124060.2{80h_CJB110}	----			
Consensus	----			

Table 88: Comparative Sequences relating to SAG0477

SEQ ID NO. 8801

STRAIN 2603

ATGCCCTAAGAAGAAATCAGATACCCAGAAAAAGAAGATTGTCTTAACGGAATGGCAA
 AAGCGTAACCTTGAATTTTAAAAAAGCGAAAGAAGATGAAGAAGAACAAAAACGTATT
 AACGAAAAATTACGCTTAGATAAAAAGAGTAAATTAATATTCTTCTCCTGAAGAACCT
 CAAATATACTACTAAAATTAAGAAGCTTCATTTTCCAAAGATTCAAGACCTAAGATTGAA
 AAGAAACAGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAATAATCGCATTAGAACT
 GCACCTATATTTGTAGTAGCATTCCTAGTCATTTAGTTCCGTTTTCCTACTAATCCT
 TTTAGTAAGCAAAAAACAAATACAGTTAGTGGAAATCAGCATACCTGATGATATTTTG
 ATAGAGAAAAACGAATATTCAAAAAACGATTAATTTCTTTCTTTAATTTTAAACATAAA
 GCTATTGAACAACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATGTCATATGCACAT
 ACAAGCAAGGATATCAACCTGTCTTGGAACTGGAAAAAGGCTGATCCTGTAAATAGT
 TCAGAGCTACCAAGCACTTCTTAACAATTAACCTTGATAAGGAAGATAGTATTAAAGCTA
 TTAATTAAAGATTAAAGGCTTTAGACCTGATTAAATAAGTGAGATTGAGGTGATAAGT
 TTAGCTGATTCTAAAACGACACCTGACCTCCTGCTGTAGATATGCACGATGGAAATAGT
 ATTAGAATACCAATTCTTAAATTTAAAGAAAGACTTCTCTTTTACAAACAAATTAAGAAG
 AACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTACACAACAACAAATACC
 ATTGAATCAACCCCTGTTAAAGCAGAAGATACAAAAATAAATCAACTGATAAAACACAA
 ACACAAATGGTTCAGGTTGCGGAAATAGTCAAGGACAAACAAATAACTCAAACTAAT
 CAACAAGGACACAGATAGCAACAGAGCAGGCACCTAACCTCAAAATGTTAAT

SEQ ID NO. 8802

STRAIN H36B

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGATT
 GTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAAGCGCAA
 AGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGATA
 AAAGAAGTAAATTAATATTCTTCTCCTGAAGAACCTCAAAATACTACT
 AAAATTAAGAAGCTTCATTTTCCAAAGATTTCAGACCTAAGATTGAAAA
 GAAACAGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAATAATCGCA
 TTAGAAGCTGACCTATATTTGTAGTAGCATTCCTAGTCATTTAGTTTCC
 GTTTTCTCTACTAATCCTTTTAGTAAGCAAAAAACAAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATATTTGTAGAGAAAAACGAATATTCAAA
 AAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
 CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
 ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAACCTGTCTTGGAACTGGAAAAAG
 GCTGATCCTGTAAATAGTTTCAAGCTACCAAGCACTTCTTAACAATTAA
 CCTTGATAAGGAAGATAGTATTAAAGCTATTAAATTAAGATTAAAGGCTT
 TAGACCTGATTAAATAAGTGAGATTGAGGTGATAAGTTTAGCTGATTCT
 AAAACGACACCTGACCTCCTGCTGTAGATATGCACGATGGAAATAGTAT
 TAGAATACCATTATCTAAATTTAAAGAAAGACTTCTCTTTTACAAACAA
 TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
 TACACAACAACAATAACCATTTGAATCAACCCCTGTTAAAGCAGAAGATAC
 AAAAAATAAATCAACTGATAAAACACAAACACAAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAAATAACTCAATACTAATCAACAAGGACAA
 CAGATAGCAACAGAGCAGGCACCTAACCTCAAAATGTTAAT

SEQ ID NO. 8803

STRAIN 18RS21

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGATT
 GTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAAGCGCAA
 AGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGATA
 AAAGAAGTAAATTAATATTCTTCTCCTGAAGAACCTCAAAATACTACT
 AAAATTAAGAAGCTTCATTTTCCAAAGATTTCAGACCTAAGATTGAAAA
 GAAACAGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAATAATCGCA
 TTAGAAGCTGACCTATATTTGTAGTAGCATTCCTAGTCATTTAGTTTCC
 GTTTTCTCTACTAATCCTTTTAGTAAGCAAAAAACAAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATATTTGTAGAGAAAAACGAATATTCAAA
 AAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
 CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
 ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAACCTGTCTTGGAACTGGAAAAAG
 GCTGATCCTGTAAATAGTTTCAAGCTACCAAGCACTTCTTAACAATTAA
 CCTTGATAAGGAAGATAGTATTAAAGCTATTAAATTAAGATTAAAGGCTT
 TAGACCTGATTAAATAAGTGAGATTGAGGTGATAAGTTTAGCTGATTCT
 AAAACGACACCTGACCTCCTGCTGTAGATATGCACGATGGAAATAGTAT
 TAGAATACCATTATCTAAATTTAAAGAAAGACTTCTCTTTTACAAACAA
 TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
 TACACAACAACAATAACCATTTGAATCAACCCCTGTTAAAGCAGAAGATAC
 AAAAAATAAATCAACTGATAAAACACAAACACAAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAAATAACTCAATACTAATCAACAAGGACAA
 CAGATAGCAACAGAGCAGGCACCTAACCTCAAAATGTTAAT

SEQ ID NO. 8804

STRAIN M732

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAG
 TTGTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAAGCGC
 AAAGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGA
 TAAAGAAGTAAATTAATATTCTTCTCCTGAAGAACCTCAAAATACTA
 CTAAAAATTAAAGAGCTTCATTTTCCAAAGATTTCAAACCTAAGATTGAA
 AAGAAACAGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAATAATCG
 CATTAGAAGTGCACCTATATTGTAGTAGCATTCCTAGTCATTTAGTTT

Table 88: Comparative Sequences relating to SAG0477

CCGTTTTCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGT
 GGAAATCAGCATACACCTGATGATATTTTGATAGAAAAACGAATATTCA
 AAAAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAAC
 AACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGC
 ATATGCACATACAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAAA
 AGGCTGATCCTGTAAATAGTTTCAGAGCTACCAAAGCACTTCTTAACAATT
 AACCTTGATAAGGAAGATAGTATTAGCTATTAAATTAAGATTAAAGGC
 TTTAGACCCTGATTAAATAAGTGAGATTCAAGGTGATAAGTTTAGCTGATT
 CTAAAAACGACACCTGACCTCCTGCTGTAGATATGCATGATGGAATAGT
 ATTAGAATACCATTTATCTAAATTTAAAGAAAGACTTCCTTTTACAAACA
 AATTAAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
 TTTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
 ACAAATAAATAAATACTGATAAAACACAAACACAAATGGTCAGGTTGC
 GGAAATAGTCAAGGACAAACAATAAATACTCAATACTAATCAACAAGGAC
 AACAGATAGCAACAGAGCAGGCACCCACCTCAAAATGTTAAT

SEQ ID NO. 8805

STRAIN COH1

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAGTT
 GTCTTAACCGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCAA
 AGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGATA
 AAAGAAGTAAATTAATATTTCTTCTCCTGAAGAACCTCAAAATACTACT
 AAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAAACCTAAGATTGAAAA
 GAAACAGAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACATAATCGCA
 TTAGAAGCTGCACCTATATTTGTAGTAGCATTCTAGTCATTTTAGTTTCC
 GTTTTCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATATTTTGATAGAAAAACGAATATTCAAA
 AAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
 CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
 ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCAT
 ATGCACATACAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAAAAG
 GCTGATCCTGTAAATAGTTTCAGAGCTACCAAAGCACTTCTTAACAATTAA
 CCTTGATAAGGAAGATAGTATTAGCTATTAAATTAAGATTAAAGGCTT
 TAGACCCTGATTAAATAAGTGAGATTCAAGGTGATAAGTTTAGCTGATTCT
 AAAACGACACCTGACCTCCTGCTGTAGATATGCATGATGGAATAGTAT
 TAGAATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTACAAACAAA
 TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
 TACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGATAC
 AAAAAATAAATAAATACTGATAAAACACAAACACAAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAATAAATACTCAATACTAATCAACAAGGACAA
 CAGATAGCAACAGAGCAGGCACCCACCTCAAAATGTTAAT

SEQ ID NO. 8806

STRAIN M781

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAG
 TTGTCTTAACCGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCG
 AAAGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGA
 TAAAGAAGTAAATTAATATTTCTTCTCCTGAAGAACCTCAAAATACTA
 CTAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAAACCTAAGATTGAA
 AAGAAACAGAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACATAATCG
 CATTAGAAGCTGCACCTATATTTGTAGTAGCATTCTAGTCATTTTAGTTT
 CCGTTTTCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGT
 GGAAATCAGCATACACCTGATGATATTTTGATAGAAAAACGAATATTCA
 AAAAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAAC
 AACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGC
 ATATGCACATACAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAAA
 AGGCTGATCCTGTAAATAGTTTCAGAGCTACCAAAGCACTTCTTAACAATT
 AACCTTGATAAGGAAGATAGTATTAGCTATTAAATTAAGATTAAAGGC
 TTTAGACCCTGATTAAATAAGTGAGATTCAAGGTGATAAGTTTAGCTGATT
 CTAAAAACGACACCTGACCTCCTGCTGTAGATATGCATGATGGAATAGT
 ATTAGAATACCATTTATCTAAATTTAAAGAAAGACTTCCTTTTACAAACA
 AATTAAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
 TTTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
 ACAAATAAATAAATACTGATAAAACACAAACACAAATGGTCAGGTTGC
 GGAAATAGTCAAGGACAAACAATAAATACTCAATACTAATCAACAAGGAC
 AACAGATAGCAACAGAGCAGGCACCCACCTCAAAATGTTAAT

SEQ ID NO. 8807

STRAIN CJB110

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAG
 TTGTCTTAACCGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCG
 AAAGAAGATGAAGAAGAACAAAAACGTATTACGAAAAATTACGCTTAGA
 TAAAGAAGTAAATTAATATTTCTTCTCCTGAAGAACCTCAAAATACTA
 CTAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAAACCTAAGATTGAA
 AAGAAACAGAAAAAGAAAAATAGTCAACAGCTTAGCCAAAACATAATCG
 CATTAGAAGCTGCACCTATATTTGTAGTAGCATTCTAGTCATTTTAGTTT
 CCGTTTTCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGT
 GGAAATCAGCATACACCTGATGATATTTTGATAGAAAAACGAATATTCA
 AAAAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAAC
 AACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGC

Table 88: Comparative Sequences relating to SAG0477

ATATGCACATACAAAGCAAGGATATCAGCCTGTCTTGAAACTGGAAAAA
 AGGCTGATCCTGTAAATAGTTCAGAGCTACCAAGCACTTCTTAACAATT
 AACCTTGATAAGGAAGATAGTATTAAAGCTATTAAATTAAGATTAAAGGC
 TTTAGACCTGATTAAATAAGTGAGATTAGGTGATAAGTTTAGCTGATT
 CTAACACGACACCTGACCTCCTGCTGTTAGATATGTCATGATGGAAATAGT
 ATTAGAATACCATTTATCTAAATTTAAAGAAAGACTTCTTTTACAAACA
 AATTAAAGAAAGCCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
 TTTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
 ACAAATAATCAACTGATATAAACACAACACAATAATGGTCAGGTTGC
 GAAAAATAGTCAAGGACAAACAAATAACTCAATACTAATCAACAAGGAC
 AACAGATAGCAACAGAGCAGGCACCCCAACCTCAAAATGTTAAT

SEQ ID NO. 8808

STRAIN 1169NT

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAAGT
 TGTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCA
 AAGAAGATGAAGAAGAACAAAAACGTATTAAACGAAAAATTACGCTTAGAT
 AAAAGAAGTAAATTAATATTTCTCTCTGAAGAACCTCAAAATACTAC
 TAAATTAAGAAAGCTTCATTTTCCAAAGATTCAAAACCTAAGATTGAAA
 AGAAACAGAAAAAAGAAAAATAGTCAACAGCTTAGCCAAACTAATCGC
 ATTAGAATCTGCACCTATATTTAGTAGCATTCTAGTTCATTTAGTTTC
 CGTTTTCTACTAATCTCTTTTAGTAAGCAAAAAACAATAACAGTTAGTG
 GAAATCAGCATACACCTGATGATATTTGATAGAGAAAAAGCAATATTCAA
 AAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACA
 ACCTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATC
 AATTTCCCAACAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCA
 TATGCACATACAAAGCAAGGATATCAGCCTGTCTTGAAACTGGAAAAA
 GGCTGATCCTGTAAATAGTTCAGAGCTACCAAGCACTTCTTAACAATTA
 ACCTTGATAAGGAAGATAGTATTAAAGCTATTAAATTAAGATTAAAGGCT
 TTAGACCTGATTAAATAAGTGAGATTAGGTGATAAGTTTAGCTGATTCT
 TAAAAACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTA
 TTAGAATACCATTTATCTAAATTTAAAGAAAGACTTCTTTTACAAACAA
 ATTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGT
 TTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGATA
 CAAAAATAAATCAACTGATATAAACACAACCCCAAAATGGTCAGGTTGCG
 GAAAAATAGTCAAGGACAAACAAATACTCAATACTAATCAACAAGGACA
 ACAACAGATAGCAACGAGCAGGCACCCCAACCTCAAAATGTTAAT

SEQ ID NO. 8809

STRAIN JM9130013

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAAGT
 GTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCA
 AGAAGATGAAGAAGAACAAAAACGTATTAAACGAAAAATTACGCTTAGATA
 AAAGAAGTAAATTAATATTTCTCTCTGAAGAACCTCAAAATACTACT
 AAAATTAAGAAAGCTTCATTTTCCAAAGATTCAAGACCTAAGATTGAAAA
 GAAACAGAAAAAAGAAAAATAGTCAACAGCTTAGCCAAACTAATCGCA
 TTAGAATCTGCACCTATATTGTAGTAGCATTCTAGTTCATTTAGTTTCC
 GTTTTCTACTAATCTCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATATTTGATAGAGAAAAAGCAATATTCAA
 AAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
 CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
 ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCAT
 ATGCACATACAAAGCAAGGATATCAACCTGTCTTGAAACTGGAAAAAAG
 CCTGATCCTGTAAATAGTTCAGAGCTACCAAGCACTTCTTAACAATTA
 CCTTGATAAGGAAGATAGTATTAAAGCTATTAAATTAAGATTAAAGGCTT
 TAGACCTGATTAAATAAGTGAGATTAGGTGATAAGTTTAGCTGATTCT
 AAAACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTAT
 TAGAATACCATTTATCTAAATTTAAAGAAAGACTTCTTTTACAAACAAA
 TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGT
 TACACAACAACAATAACCATTTGAATCAACCCCTGTTAAAGCAGAAGATAC
 AAAAAATAAATCAACTGATATAAACACAACACAATAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAAATACTCAATACTAATCAACAAGGACAA
 CAGATAGCAACAGAGCAGGCACCTAACCTCAAAATGTTAAT

SEQ ID NO. 8810

STRAIN A909

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAAGTGTCT
 TTAACGGAATGGCAAAAGCGTAACCTTGAATTTTaaAAAAACGCAAGA
 AGATGAAGAAGAAaCAAAAAACGTATTAAACGAAAAATTACGCTTAGATAAAA
 GAAGTAAATTAATATTTCTCTCTGAAGAACCTCAAAATACTACTATAA
 ATTAAGAAAGCTTCATTTTCCAAAGATTCAAGACCTAAGATTGAAAAGAA
 ACAGAAAAAAGAAAAATAGTCAACAGCTTAGCCAAACTAATCGCATTA
 GAATGACACCTATATTGTAGTAGCATTCTAGTTCATTTAGTTTCCGTT
 TTCTCTAATCTCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGGAAA
 TCAGCATACACCTGATGATATTTGATAGAGAAAAAGCAATATTCAAAAAA
 ACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAACGT
 TTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCAATT
 TCCCAATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCATATG
 CACATACAAAGCAAGGATATCAACCTGTCTTGAAACTGGAAAAAAGGCT
 GATCCTGTAAATAGTTCAGAGCTACCAAGCACTTCTTAACAATTAACCT
 TGATAAGGAAGATAGTATTAAAGCTATTAAATTAAGATTAAAGGCTTTAG
 ACCTGATTTAATAAGTGAGATTAGGTGATAAGTTTAGCTGATTCTAAA
 ACGACACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTATTAA

Table 88: Comparative Sequences relating to SAG0477

AATACCATTATCTAAATTTAAAGAAAGACTTCCTTTTACAAACAAATTA
 AGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTAC
 ACAACAACAAATACCATTGAATCAACCCCTGTTAAAGCAGAAGATACAAA
 AAATAAATCAACTGATAAAACAAACCAAAATGGTCAGGTTGCGGAAA
 ATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAAGGACAACAG
 ATAGCAACAGAGCAGGCACCTAACCTCAAATGTTAAT

SEQ ID NO. 8811

STRAIN 090

TAAGAAGAAATCAGATACCCAGAAAAAGAAGTTGTCTTAACGGAAT
 GGCAAAAGCGTAACCTTGAATTTTAAAAAACGCAAGAAGATGAAGAA
 GAACAAAACGTTATTAACGAAAAATACGCTTAGATAAAAGAAGTaaATT
 AAATATTCTTCTCCTGAAGAACCTCAAATACTACTAAAATTAGAAGC
 TTCATTTTCCAAGATTTCAAAACCTAAGATTGAAAAGAAACGAAAAAA
 GAAAAAATAGTCAACAGCTTAGCCAAAATTAATCGCATTAGAAGTGCACC
 TATATTGTTAGTAGCATTCTTAGTCATTTTAGTTTCCGTTTCTACTAA
 CTCTTTTAGTAAGCAAAAACATAACAGTTAGTGGAAATCAGCATACA
 CCTGATGATATTTTGATAGAAAAACGAATATTCAAAAAACGATTATTT
 CTTTCTTTAATTTTAAACATAAAGCTATTGAACAACGTTTAGCTGCAG
 AAGATGTATGGGTAACAGCTCAGATGACTTATCAATTTCCCAATAAG
 TTTCAATTTCAAGTTCAAGAAAAATAAGATTATTGCATATGCACATACAAA
 GCAAGGATATCAGCCTGTCTTGAAACTGGAAGAAAGGCTGATCCTGTAA
 ATAGTTTCAGAGCTACCAAGCACTTCTTAACAATTAACCTTGATAAGGAA
 GATAGTATTAAGCTATTAATTAAGATTAAAGGCTTAGACCTGATTT
 AATAAGTGAGATTCAAGGTGATAAGTTTAGCTGATTCTAAAACGACCTG
 ACCTCCTGCTGTTAGATATGATGATGGAATAGTATTAGAATACCATTA
 TCTAAATTTAAAGAAAGACTTCTCTTTTACAAACAAATTAAGAAGAACTT
 TAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTACACAACAACAA
 GTACTATTGAATCAACCCCTGTGAAAGCGGAAGATACAAAAATAAATCA
 ACTGATATAAACACAAACCAAAATGGTCAGGTTGCGGAAAATAGTCAAGG
 ACAACAAATAACTCAAATACTAATCAACAAGGACAACAGATGCAACAG
 AGCAGGCACCAACCTCAAATGTTAAT

PRETTY of: /biotmp/msa24691.2{*} August 5, 2002 05:14 ..

	1	50
msa252409.2{85_090.con}	~~TAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_CJB110}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_COH1}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_M732}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_M781}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_18RS21}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_2603}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_A909}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_H36B}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_JM9130013}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
msa252409.2{85_1169NT}	CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA	
Consensus	*****	*****
	51	100
msa252409.2{85_090.con}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_CJB110}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_COH1}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_M732}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_M781}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_18RS21}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_2603}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_A909}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_H36B}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_JM9130013}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
msa252409.2{85_1169NT}	ATGGCAAAAG CGTAACCTTG AATTTTTTAA AAAACGCAAA GAAGATGAAG	
Consensus	*****	*****
	101	150
msa252409.2{85_090.con}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_CJB110}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_COH1}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_M732}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_M781}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_18RS21}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_2603}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_A909}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_H36B}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_JM9130013}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_1169NT}	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
Consensus	*****	*****
	151	200
msa252409.2{85_090.con}	TTAAATATTT CTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA	
msa252409.2{85_CJB110}	TTAAATATTT CTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA	
msa252409.2{85_COH1}	TTAAATATTT CTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA	
msa252409.2{85_M732}	TTAAATATTT CTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA	

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_M781}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_18RS21}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_2603}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_A909}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_H36B}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_JM9130013}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_1169NT}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
Consensus	*****	*****	*****	*****	*****
201					
msa252409.2{85_090.con}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_CJB110}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_COH1}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_M732}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_M781}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_18RS21}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_2603}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_A909}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_H36B}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_JM9130013}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_1169NT}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
Consensus	*****	*****	***-*****	*****	*****
251					
msa252409.2{85_090.con}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_CJB110}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_COH1}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_M732}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_M781}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_18RS21}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_2603}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_A909}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_H36B}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_JM9130013}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_1169NT}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAACTGCA
Consensus	*****	*****	*****	*****	*****
301					
msa252409.2{85_090.con}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_CJB110}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_COH1}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_M732}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_M781}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_18RS21}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_2603}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_A909}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_H36B}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_JM9130013}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
msa252409.2{85_1169NT}	CCTATATTTa	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCTTACT
Consensus	*****	*****	*****	*****	*****
351					
msa252409.2{85_090.con}	AACCTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_CJB110}	AACCTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_COH1}	AACCTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_M732}	AACCTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_M781}	AACCTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_18RS21}	AACCTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_2603}	AACCTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_A909}	AACCTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_H36B}	AACCTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_JM9130013}	AACCTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_1169NT}	AACCTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
Consensus	*****	*****	*****	*****	*****
401					
msa252409.2{85_090.con}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_CJB110}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_COH1}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_M732}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_M781}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_18RS21}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_2603}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_A909}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_H36B}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_JM9130013}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_1169NT}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
Consensus	*****	*****	***-*****	*****	*****
451					
msa252409.2{85_090.con}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_CJB110}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_COH1}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_M732}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
msa252409.2{85_M781}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
msa252409.2{85_18RS21}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
msa252409.2{85_2603}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
msa252409.2{85_A909}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
msa252409.2{85_H36B}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
msa252409.2{85_JM9130013}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
msa252409.2{85_1169NT}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC		
Consensus	*****	*****	*****	*****	*****		
msa252409.2{85_090.con}	501	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa	550
msa252409.2{85_CJB110}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa		
msa252409.2{85_COH1}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa		
msa252409.2{85_M732}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa		
msa252409.2{85_M781}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa		
msa252409.2{85_18RS21}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa		
msa252409.2{85_2603}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa		
msa252409.2{85_A909}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa		
msa252409.2{85_H36B}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa		
msa252409.2{85_JM9130013}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa		
msa252409.2{85_1169NT}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa		
Consensus	*****	*****	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	551	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA	600
msa252409.2{85_CJB110}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA		
msa252409.2{85_COH1}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA		
msa252409.2{85_M732}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA		
msa252409.2{85_M781}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA		
msa252409.2{85_18RS21}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA		
msa252409.2{85_2603}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA		
msa252409.2{85_A909}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA		
msa252409.2{85_H36B}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA		
msa252409.2{85_JM9130013}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA		
msa252409.2{85_1169NT}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA		
Consensus	*****	*****	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	601	AAGCAAGGAT	ATCAGCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT	650
msa252409.2{85_CJB110}	AAGCAAGGAT	ATCAGCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT		
msa252409.2{85_COH1}	AAGCAAGGAT	ATCAGCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT		
msa252409.2{85_M732}	AAGCAAGGAT	ATCAGCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT		
msa252409.2{85_M781}	AAGCAAGGAT	ATCAGCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT		
msa252409.2{85_18RS21}	AAGCAAGGAT	ATCAGCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT		
msa252409.2{85_2603}	AAGCAAGGAT	ATCAGCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT		
msa252409.2{85_A909}	AAGCAAGGAT	ATCAGCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT		
msa252409.2{85_H36B}	AAGCAAGGAT	ATCAGCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT		
msa252409.2{85_JM9130013}	AAGCAAGGAT	ATCAGCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT		
msa252409.2{85_1169NT}	AAGCAAGGAT	ATCAGCCTGT	CTTGGAAACT	GGAAAAAAGG	CTGATCCTGT		
Consensus	*****	*****	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	651	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG	700
msa252409.2{85_CJB110}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG		
msa252409.2{85_COH1}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG		
msa252409.2{85_M732}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG		
msa252409.2{85_M781}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG		
msa252409.2{85_18RS21}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG		
msa252409.2{85_2603}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG		
msa252409.2{85_A909}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG		
msa252409.2{85_H36B}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG		
msa252409.2{85_JM9130013}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG		
msa252409.2{85_1169NT}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG		
Consensus	*****	*****	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	701	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCGTGAT	750
msa252409.2{85_CJB110}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCGTGAT		
msa252409.2{85_COH1}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCGTGAT		
msa252409.2{85_M732}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCGTGAT		
msa252409.2{85_M781}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCGTGAT		
msa252409.2{85_18RS21}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCGTGAT		
msa252409.2{85_2603}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCGTGAT		
msa252409.2{85_A909}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCGTGAT		
msa252409.2{85_H36B}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCGTGAT		
msa252409.2{85_JM9130013}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCGTGAT		
msa252409.2{85_1169NT}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCGTGAT		
Consensus	*****	*****	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	751	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC	800
msa252409.2{85_CJB110}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC		

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_COH1}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_M732}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_M781}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_18RS21}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_2603}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_A909}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_H36B}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_JM9130013}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_1169NT}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_CJB110}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_COH1}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_M732}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_M781}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_18RS21}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_2603}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_A909}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_H36B}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_JM9130013}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
msa252409.2{85_1169NT}	TGACCTCCTG	CTGTTAGATA	TGCATGATGG	AAATAGTATT	AgaATACCAT
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_CJB110}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_COH1}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_M732}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_M781}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_18RS21}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_2603}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_A909}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_H36B}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_JM9130013}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_1169NT}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTT	ACAAACAAAT	TAAGAAGAAC
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_CJB110}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_COH1}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_M732}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_M781}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_18RS21}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_2603}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_A909}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_H36B}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_JM9130013}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_1169NT}	CTTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
msa252409.2{85_CJB110}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
msa252409.2{85_COH1}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
msa252409.2{85_M732}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
msa252409.2{85_M781}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
msa252409.2{85_18RS21}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT
msa252409.2{85_2603}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT
msa252409.2{85_A909}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT
msa252409.2{85_H36B}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT
msa252409.2{85_JM9130013}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT
msa252409.2{85_1169NT}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
Consensus	**--***--***	*****	****-*****	-*****	*****
msa252409.2{85_090.con}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_CJB110}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_COH1}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_M732}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_M781}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_18RS21}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_2603}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_A909}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_H36B}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_JM9130013}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_1169NT}	CAACTGATAA	AACACAAaCc	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
Consensus	*****	*****-*	*****	*****	*****
msa252409.2{85_090.con}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_CJB110}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_COH1}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_M732}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_M781}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_18RS21}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_2603}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_A909}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_H36B}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_JM9130013}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_1169NT}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGGacaAC	AACAGATAGC
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	1101				1134
msa252409.2{85_CJB110}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
msa252409.2{85_COH1}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
msa252409.2{85_M732}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
msa252409.2{85_M781}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
msa252409.2{85_18RS21}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
msa252409.2{85_2603}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
msa252409.2{85_A909}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
msa252409.2{85_H36B}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
msa252409.2{85_JM9130013}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
msa252409.2{85_1169NT}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT	TAAT	
Consensus	***-*****	*****-****	*****	****	

SEQ ID NO. 8812

STRAIN 2603 frame: 1

PKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEBPQ
NTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPIFVVAFLVILVSVFLLTPF
SKQKTIITVSGNQHTPPDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIVQVENKI IAYAHTKQGYQPVLETGKKADPNVNSSELPHKFLTINLDKEDSIKLL
IKDLKALDPDLISEIQVLSLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
LKEPSIVDMEVGVTITNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNNTNQ
QGQQIATEQAPNPQNVN

SEQ ID NO. 8813

STRAIN H36B frame: 1

PKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEBPQ
NTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPIFVVAFLVILVSVFLLTPF
SKQKTIITVSGNQHTPPDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIVQVENKI IAYAHTKQGYQPVLETGKKADPNVNSSELPHKFLTINLDKEDSIKLL
IKDLKALDPDLISEIQVLSLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
LKEPSIVDMEVGVTITNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNNTNQ
QGQQIATEQAPNPQNVN

SEQ ID NO. 8814

STRAIN 18RS21 frame: 1

PKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEBPQ
NTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPIFVVAFLVILVSVFLLTPF
SKQKTIITVSGNQHTPPDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIVQVENKI IAYAHTKQGYQPVLETGKKADPNVNSSELPHKFLTINLDKEDSIKLL
IKDLKALDPDLISEIQVLSLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
LKEPSIVDMEVGVTITNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNNTNQ
QGQQIATEQAPNPQNVN

SEQ ID NO. 8815

STRAIN M732 frame: 1

PKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEBPQ
NTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPIFVVAFLVILVSVFLLTPF
SKQKTIITVSGNQHTPPDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIVQVENKI IAYAHTKQGYQPVLETGKKADPNVNSSELPHKFLTINLDKEDSIKLL
IKDLKALDPDLISEIQVLSLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
LKEPSIVDMEVGVTITNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNNTNQ
QGQQIATEQAPNPQNVN

SEQ ID NO. 8816

STRAIN COH1 frame: 1

PKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEBPQ
NTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRI RTAPIFVVAFLVILVSVFLLTPF
SKQKTIITVSGNQHTPPDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIVQVENKI IAYAHTKQGYQPVLETGKKADPNVNSSELPHKFLTINLDKEDSIKLL
IKDLKALDPDLISEIQVLSLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
LKEPSIVDMEVGVTITNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNNNTNQ
QGQQIATEQAPNPQNVN

SEQ ID NO. 8817

STRAIN M781 frame: 1

PKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPPEBPQ

Table 88: Comparative Sequences relating to SAG0477

NTTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 SKQKTTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPLDISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKSDDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8818

STRAIN CJB110 frame: 1

PKKKSDDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
 NTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 SKQKTTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPLDISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKSDDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8819

STRAIN 1169NT frame: 1

PKKKSDDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
 NTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 SKQKTTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPLDISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKSDDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8820

STRAIN JM9130013 frame: 1

PKKKSDDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
 NTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 SKQKTTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPLDISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVYTTTNTIESTPVKAEDTKNKSDDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8821

STRAIN A909 frame: 1

PKKKSDDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
 NTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 SKQKTTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 FPNKFHIQVQENKI IAYAHKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
 IKDLKALDPLDISEIQVISLADSKTTPDLLLLDMHDGNSIXIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVYTTTNTIESTPVKAEDTKNKSDDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8822

STRAIN 090 frame: 2

KKKSDDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
 TTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
 KQKTTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
 PKNKFHIQVQENKI IAYAHKQGYQPVLETGKKADPVNSSELPHFLTINLDKEDSIKLLI
 KDLKALDPLDISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKNL
 KEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKSDDKTQTQNGQVAENSQGGTNNNTNQ
 QGQQIATEQAPNPQNVN

PRETTY of: /biotmp/msa252337.2{*} January 31, 2003 03:32 ..

	1		50
msa252337.2{85_090}	-KKKSDDTPEK	EEVVLTEWQK	RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_18RS21}	PKKKSDDTPEK	EEVVLTEWQK	RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_2603}	PKKKSDDTPEK	EEVVLTEWQK	RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_A909}	PKKKSDDTPEK	EEVVLTEWQK	RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_CJB110}	PKKKSDDTPEK	EEVVLTEWQK	RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_COH1}	PKKKSDDTPEK	EEVVLTEWQK	RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_H36B}	PKKKSDDTPEK	EEVVLTEWQK	RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_JM9130013}	PKKKSDDTPEK	EEVVLTEWQK	RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_M732}	PKKKSDDTPEK	EEVVLTEWQK	RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_M781}	PKKKSDDTPEK	EEVVLTEWQK	RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
msa252337.2{85_1169NT}	PKKKSDDTPEK	EEVVLTEWQK	RNLEFLKKRK EDEEEQKRIN EKLRLDKRSK
Consensus	*****	*****	*****
	51		100
msa252337.2{85_090}	LNISSPEEPQ	NTTKIKKLHF	PKISrPKIEK QKQKEKIVNS LAKTNRIRTA
msa252337.2{85_18RS21}	LNISSPEEPQ	NTTKIKKLHF	PKISrPKIEK QKQKEKIVNS LAKTNRIRTA
msa252337.2{85_2603}	LNISSPEEPQ	NTTKIKKLHF	PKISrPKIEK QKQKEKIVNS LAKTNRIRTA
msa252337.2{85_A909}	LNISSPEEPQ	NTTKIKKLHF	PKISrPKIEK QKQKEKIVNS LAKTNRIRTA
msa252337.2{85_CJB110}	LNISSPEEPQ	NTTKIKKLHF	PKISrPKIEK QKQKEKIVNS LAKTNRIRTA

Table 88: Comparative Sequences relating to SAG0477

msa252337.2{85_COH1}	LNISSPPEEPQ	NTTKIKKLHF	PKISkPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_H36B}	LNISSPPEEPQ	NTTKIKKLHF	PKISrPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_JM9130013}	LNISSPPEEPQ	NTTKIKKLHF	PKISrPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_M732}	LNISSPPEEPQ	NTTKIKKLHF	PKISkPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_M781}	LNISSPPEEPQ	NTTKIKKLHF	PKISkPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_1169NT}	LNISSPPEEPQ	NTTKIKKLHF	PKISkPKIEK	KQKKEKIVNS	LAKTNRIRTA
Consensus	*****	*****	****_****	*****	*****
msa252337.2{85_090}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_18RS21}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_2603}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_A909}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_CJB110}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_COH1}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_H36B}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_JM9130013}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_M732}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_M781}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_1169NT}	PIFvVAFVLVI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
Consensus	***_****	*****	*****	*****	*****
msa252337.2{85_090}	FFSLIFKHKA	IEQRLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_18RS21}	FFSLIFKHKA	IEQRLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_2603}	FFSLIFKHKA	IEQRLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_A909}	FFSLIFKHKA	IEQRLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_CJB110}	FFSLIFKHKA	IEQRLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_COH1}	FFSLIFKHKA	IEQRLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_H36B}	FFSLIFKHKA	IEQRLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_JM9130013}	FFSLIFKHKA	IEQRLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_M732}	FFSLIFKHKA	IEQRLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_M781}	FFSLIFKHKA	IEQRLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_1169NT}	FFSLIFKHKA	IEQRLAAEDV	WVKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
Consensus	*****	*****	*****	*****	*****
msa252337.2{85_090}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_18RS21}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_2603}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_A909}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_CJB110}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_COH1}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_H36B}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_JM9130013}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_M732}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_M781}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_1169NT}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
Consensus	*****	*****	*****	*****	*****
msa252337.2{85_090}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFYKQIKKN
msa252337.2{85_18RS21}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFYKQIKKN
msa252337.2{85_2603}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFYKQIKKN
msa252337.2{85_A909}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	xIPLSKFKER	LPFYKQIKKN
msa252337.2{85_CJB110}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFYKQIKKN
msa252337.2{85_COH1}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFYKQIKKN
msa252337.2{85_H36B}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFYKQIKKN
msa252337.2{85_JM9130013}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFYKQIKKN
msa252337.2{85_M732}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFYKQIKKN
msa252337.2{85_M781}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFYKQIKKN
msa252337.2{85_1169NT}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LPFYKQIKKN
Consensus	*****	*****	*****	-*****	*****
msa252337.2{85_090}	LKEPSIVDME	GVVYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_18RS21}	LKEPSIVDME	GVVYTTTnTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_2603}	LKEPSIVDME	GVVYTTTnTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_A909}	LKEPSIVDME	GVVYTTTnTI	ESTPVKAEDT	KNKSTDKTQx	QNGQVAENSQ
msa252337.2{85_CJB110}	LKEPSIVDME	GVVYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_COH1}	LKEPSIVDME	GVVYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_H36B}	LKEPSIVDME	GVVYTTTnTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_JM9130013}	LKEPSIVDME	GVVYTTTnTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_M732}	LKEPSIVDME	GVVYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_M781}	LKEPSIVDME	GVVYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_1169NT}	LKEPSIVDME	GVVYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
Consensus	*****	*****_**	*****	*****_	*****
msa252337.2{85_090}	GQTNNNSNTNQ	QGQQiatega	pnpqnv-		
msa252337.2{85_18RS21}	GQTNNNSNTNQ	QGQQiatega	pnpqnv-		
msa252337.2{85_2603}	GQTNNNSNTNQ	QGQQiatega	pnpqnv-		
msa252337.2{85_A909}	GQTNNNSNTNQ	QGQQiatega	pnpqnv-		

Table 88: Comparative Sequences relating to SAG0477

msa252337.2{85_CJB110}	GQTNNSENTNQ	QGQQiateqa	pnpqnv~
msa252337.2{85_COH1}	GQTNNSENTNQ	QGQQiateqa	pnpqnv~
msa252337.2{85_H36B}	GQTNNSENTNQ	QGQQiateqa	pnpqnv~
msa252337.2{85_JM9130013}	GQTNNSENTNQ	QGQQiateqa	pnpqnv~
msa252337.2{85_M732}	GQTNNSENTNQ	QGQQiateqa	pnpqnv~
msa252337.2{85_M781}	GQTNNSENTNQ	QGQQiateqa	pnpqnv~
msa252337.2{85_1169NT}	GQTNNSENTNQ	QGQQiateq	apnpqnv~
Consensus	*****	****~	~

Table 89: Comparative Sequences relating to SAG1350

SEQ ID NO. 8901

STRAIN 2603

ATGAAAAAGGACAAAGTAAATGATACTAAGCAATCTTACTCTCTACGTAAA
 TATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTACATAATGGTCACAACTCCTGTT
 TTTGCGGATCAAACATACATCGGTTCAAGTTAATAATCAGACAGGCCTAGTGTGGATGCT
 AATAATTCCTCCAATGAGACAAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGT
 CAAGCGTCTGATAAAGTTGTAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCT
 TTAGTAGAGACAAAGCCAAATGGTGGAAAAACATTACCTGAACAAGGGAATTTATGTTTAT
 AGCAAGAAACCGAGGTGAAAAATACACCTTCAAATCAGCCCCAGTAGCTTTCTATGCA
 AAGAAAGGTGATAAAGTTTCTATGACCAAGTATTTAATAAAGATAATGTGAAATGGATT
 TCATATAAGTCTTTTGTGGCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCA
 GGAGGTTTCAAGACTAAAGCACCTACTCCTGTAAACAAATTCAGGAAGCAATAATCAAGAG
 AAAATAGCAACGCAAGGAAATTTATACATTTTCACATAAAGTAGAAGTAAAAAATGAAGCT
 AAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGAGACAGAATTTTTTACGACCAA
 ATACTAATCTATTGAAGGAAATCAGTGGTTATCTTATAAATCAITCAATGGTGTTCGTCGT
 TTTGTTTGTCTAGGTAAAGCATCTTCACTAGAAAAAATGAAGATAAAGAAAAAGTGTCT
 CCTCAACCACAAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAACT
 ACAGGTTTTGATATTTTAAATACGAATATTAAAGATGATAACGGTATCGTGTCTGTTAAG
 GTACCGGTTTGGACTGAACAAGGAGGCAAGATGATATTAAATGGTATACAGCTGTAAT
 ACTGGGGATGGCAACTACAAAGTAGCTGTATCATTTGCTGACCATAAGAATGAGAAGGGT
 CTTTATAATATTCTTTTACTACCAAGAGCTAGTGGGACACTTGTAGGTGTAAACAGGA
 ACTAAAGTGACAGTAGCTGGAACTAATTTCTCTCAAGAACCTATTGAAAAAGGTTTAGCA
 AAGACTGGTGTTTTAAATATTATCGGAAGTACTGAAGTAAAAAATGAAGCTAAAAATATCA
 AGTCAGACCCAAATTTACTTTAGAAAAAGGTGACAAAAATAAATATGATCAAGTATTGACA
 GCAGATGGTTTACCAGTGGATTCTTACAAATCTTATAGTGGTGTTCGTGCTATATTCCT
 GTGAAAAAGCTAACTACAGTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGT
 TATCCCACTTACCTTAAACAGGTACCTATACATTTACTAAAACCTGTAGATGTGAAAAAGT
 CAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGA AAAAATACATTAT
 GATCAAGTGTTAGTAGTAGATGGTTCATCAGTGGATTTTCATACAAGAGTTATTCCGGTATT
 CGTCGCTATATTGAAAT

SEQ ID NO. 8902

STRAIN 090

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTTACT
 CTCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATT
 ATAATGGTCACAAGTCTGTTTGTGCGGATCAAACATACATCGGTTCAAGT
 TAATAATCAGACAGGCCTAGTGTGGATGCTAATAATCTTCCAATGAGA
 CAAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCT
 GATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCC
 TTTAGTAGAGACAAAGCCAAATGGTGGAAAAACATTACCTGAACAAGGGA
 ATTATGTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAATCA
 GCCCCAGTAGCTTTCTATGCAAAAGAAAGGTGATAAAGTTTCTATGACCA
 AGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTTGTG
 GCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTCA
 GAGACTAAAGCACCTACTCCTGTAAACAAATTCAGGAAGCAATAATCAAGA
 GAAAAATAGCAACGCAAGGAAATATACATTTTCATATAAGTAGAAGTAA
 AAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGA
 ACAGAAATTTTACGACCAAAATACTAATTTGAAGGAAATCAGTGGTT
 ATCTTATAAATCAITCAATGGTGTTCGTGTTTGTCTAGGTAAAG
 CATCTTCAGTAGAAAAAATGAAGATAAAGAAAAAGTGTCTCCTCAACCA
 CAAGCCCGTATTACTAAAACTGGTAGACTGACTATTTCTAACGAAACAACT
 TACAGGTTTTGATATTTAATTACGAATATTAAAGATGATAACGGTATCG
 CTGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGCAAGATGATATT
 AAATGGTATACAGCTGTAACTACTGGGGATGGCACTACAAAGTAGCTGT
 ATCATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCAITTTAT
 ACTACCAAGAGCTAGTGGGACACTTGTAGGTGTAAACAGGAACATAAGTG
 ACAGTAGCTGGAACCTAATCTTCTCAAGAACCTATTGAAATGGTTTAGC
 AAAGACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAATGAAG
 CTAAAAATATCAAGTCAAGTCAAGCCCAATTTACTTTAGAAAAAGGTGACAAAAATA
 AATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACAA
 ATCTTATAGTGGTGTTCGTGCTATATTCCTGTGAAAAAGCTAACTACAA
 GTAGTGA AAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAAC
 TTACCTAAAAAGGTACCTATACATTTACTAAAACTGTAGATGTGAAGAG
 TCAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTCAAAGGGTGA
 AAATACATTATGATCAAGTGTAGTAGTAGATGGTTCATCAGTGGATTTCA
 TACAAGAGTTATTCGGTATTCGTGCTATATTGAAAT

SEQ ID NO. 8903

STRAIN A909

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTTAC
 TCCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATT
 CATATAATGGTCACAAGTCTGTTTGTGCGGATCAAACATACATCGGTTCAAG
 TTAATAATCAGACAGGCCTAGTGTGGATGCTAATAATCTTCCAATGAG
 ACAAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCT
 TGATAAAGTTGTAATAGTCAAAATACGGCAACAAAGGACATTACTACTC
 CTTTAGTAGAGACAAAGCCAAATGGTGGAAAAACATTACCTGAACAAGGG
 AATTATGTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAATC
 AGCCCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTCTATGACC
 AAGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTTGT
 GGCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTT
 AGAGACTAAAGCACCTACTCCTGTAAACAAATTCAGGAAGCAATAATCAAG
 AGAAAAATAGCAACGCAAGGAAATTTATACATTTTCACATAAAGTAGAAGTA
 AAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGG

Table 89: Comparative Sequences relating to SAG1350

AGACAGAATTTTTTACGACCAAATACTAATCTATTGAAGGAAATCAGTGGT
TATCTTATAAATCATTCAATGGTGTTCGTGTTTTGTTTGCTAGGTAAA
GCATCTTCAGTAGAAAAAAGCTGAAGATAAAGAAAAAGTGTCTCCTCAACC
ACAAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAA
CTACAGGTTTTGATATTTAATTACGAATATTAAGATGATAACGGTATC
GCTGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATAT
TAAATGGTATACAGCTGTAACTACTGGGATGGCAACTACAAAGTAGCTG
TATCATTTGCTGACCATAAGAAATGAGAAGGGTCTTTATAATATTCAATTA
TACTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAGT
GACAGTAGCTGGAATAATCTTCTCAAGAACCTATTGAAATGGTTTAG
CAAAGACTGGTGTATTATAATATTATCGGAAGTACTGAAGTAAAAAATGAA
GCTAAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAAAT
AAATTTATGATCAAGTATTGACAGCAGATGGTTACAGTGGATTCTTACA
AATCTTATAGTGGTGTTCGTGCTATATTCTGTGAAAAAGCTAACTACA
AGTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAA
CTTACCTAAAACAGGTACCTATACATTTACTAAAACCTGTAGATGTGAAGA
GTCACCTAAAAGTATCAAGTCCAGTGGAAATTAATTTTCAAAGGGTGAA
AAAAATACATTATGATCAAGTGTAGTAGATGGTCATCAGTGGATTTC
ATACAAGAGTTATTCCGGTATTCTGTCGTATATTGAAATT

SEQ ID NO. 8904

STRAIN H36B

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACT
CTCTACGTAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTTC
ATAATGGTCAACAAGTCTGTGTTTGGCGATCAAACTACATCGGTTCAAGT
TAATAATCAGACAGGCACTAGTGTGGATGATAAATTTCTTCAATGAGA
CAAGTCGCTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCGTCT
GATAAAGTTGTAATAGTCAAAATACGGCAACAAAGGACATTACTACTCC
TTTAGTAGAGACAAAGCCAATGGTGGAAAAACATTACCTGAACAAGGGA
ATTATGTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAAATCA
GCCCCAGTAGCTTTCTATGCAAGAAGGATGATAAAGTTTCTATGACCA
AGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTGTG
GCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTCA
GAGACTAAAGCACCTACTCTGTAAACAAATTCAGGAAGCAATAATCAAGA
GAAAAATAGCAACGCAAGGAAATATACATTTTACATAAAGTAGAAGTAA
AAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGA
GACAGAATTTTTTACGACCAAAATACTAATTTGAAGGAAATCAGTGGTT
ATCTTATAAATCATTCAATGGTGTTCGTGTTTTGTTTGCTAGGTAAAG
CATCTTCAGTAGAAAAAAGCTGAAGATAAAGAAAAAGTGTCTCCTCAACCA
CAAGCCGCTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAA
TACAGGTTTTGATATTTAATTACGAATATTAAAGATGATAACGGTATCG
CTGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATT
AAATGGTATACAGCTGTAACCTACTGGGATGGCAACTACAAAGTAGCTGT
ATCATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAATATTCAATTAT
ACTACCAAGAAAGCTAGTGGGACACTTGTAGGTGTAACAGCACTAAAGTG
ACAGTAGCTGGAACTAATCTTCTCAAGAACCTATTGAAAATGGTTTAGC
AAAGACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAG
CTAAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAAATA
AATTATGATCAAGTATTGACAGCAGATGGTTACAGTGGATTCTTACAA
ATCTTATAGTGGTGTTCGTGCTATATTCTGTGAAAAAGCTAACTACAA
GTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAAC
TTACCTAAAACAGGTACCTATACATTTACTAAAACCTGTAGATGTGAAGAG
TCAACCTAAAGTATCAAGTCCAGTGGAAATTAATTTTCAAAGGGTGAAA
AAATACATTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTTC
TACAAGAGTTATTCCGGTATTCTGTCGTATATTGAAATT

SEQ ID NO. 8905

STRAIN 18RS21

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTC
TCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTCA
TAATGGTCAACAAGTCTGTGTTTGGCGATCAAACTACATCGGTTCAAGTT
AATAATCAGACAGGCACTAGTGTGGATGCTAATAATCTTCCAATGAGAC
AAGTGGCTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCGTCTG
ATAAAGTTGTAATAAGTCAAAATACGGCAACAAAGGACATTACTACTCT
TTAGTAGAGACAAAGCCAATGGTGGAAAAACATTACCTGAACAGGGAA
TTATGTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAAATCAG
CCCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTCTATGACCAA
GTATTTAATAAAGATAATGTGAATGGATTTCATATAAGTCTTTTGTGG
CGTAGCTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTGAG
AGACTAAAGCACCTACTCTGTAAACAAATTCAGGAAGCAATAATCAAGAG
AAAATAGCAACGCAAGGAAATATACATTTTACATAAAGTAGAAGTAAA
AAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGCAAAAGGAG
ACAGAATTTTTTACGACCAAAATACTAATTTGAAGGAAATCAGTGGTTA
TCTTATAAATCATTCAATGGTGTTCGTGTTTTGTTTGCTAGGTAAAGC
ATCTTCAGTAGAAAAAAGTGAAGATAAAGAAAAAGTGTCTCTCAACCAC
AAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAACT
ACAGGTTTGTATATTTAATTACGAATATTAAAGATGATAACGGTATCGC
TGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATTA
AATGGTATACAGCTGTAACCTACTGGGATGGCAACTACAAAGTAGCTGTA
TCATTTGCTGACCATAAGAATGAGAAGGTCTTTATAATATTCAATTTATA
CTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAGTGA
CAGTAGCTGGAACATAATCTTCTCAAGAACCTATTGAAAAAGTTTAGCA
AAGACTGGTGTATTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAGC

Table 89: Comparative Sequences relating to SAG1350

TAAAAATCAAGTCAGACCCCAATTTACTTTAGAAAAAGGTGACAAAATAA
 ATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACAAA
 TCTTATAGTGGTTCGTCGTATATTCCTGTGAAAAAGCTAACTACAAG
 TAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACT
 TACCTAAAACAGGTACCTATACATTTACTAAAACGTAGATGTGAAAAGT
 CAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAAGGGTGAAAA
 AATACATTTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTTTCAT
 ACAAGAGTTATTCCGGTATTTCGTTCGTATATTGAAATT

SEQ ID NO. 8906

STRAIN M732

CAAGTAAATGATaCTAAGCAATCTTACTCTCTACGTAAATATAAATTGCG
 TTTAGCATCAGTAATTTTAGGGTCATTCTAATGGTCACAAGTCCGTGTTT
 TTGCGGATCAAACTACATCGGTTCAAGTTAATAATCAGACAGGCACTAGT
 GTGGATGCTAATAATTCTTCCAATGAGACAAGTCCGTCAAGTGTGATTAC
 TTCCAATATGATAGTGTTCAGCGCTCGATAAAGTTGTAAATAGTCAAA
 ATACGGCAACAAAGGACATTACTACTCCTTTAGTAGAGACAAAGCCAATG
 GTGGAAAAACATTTACCTGAACAAGGGAATTATGTTTATAGCAAGAAAC
 CGAGGTGAAAAATACACCTTCAAAATCAGCCCCAGTAGCTTTCTATGCAA
 AGAAAGGTGATAAAGTTTCTATGACCAAGTATTTAATAAAGATAATGTG
 AAATGGATTTATATAAGTCTTTTGGTGGCGTACGTGATACGCAGCTAT
 TGAGTCACTAGATCCATCAGGAGGTTTCAAGAGACTAAAGCACCTACTCCTG
 TAACAAATTCAGGAAGCAATAATCAAGAGAAAAATAGCAACGCAAGGAAAT
 TATACATTTTACATAAAGTAGAAGTAAAAATGAAGCTAAGGTAGCGAG
 TCCAATCAATTTTACATTTGGACAAAGGAGACAGAATTTTACGACCAAA
 TACTAATCTATGAAGGAAATCAGTGGTTATCTTATAAATCATTCATGGT
 GTTCGTGCTTTTGTCTTGGTAAAGCATCTTCAGTAGAAAAAACTGA
 AGATAAAGAAAAAGTGTCTCTCAACCACAAGCCGTATTACTAAAACCTG
 GTAGACTGACTATTTCTAACGAAACAACTACAGGTTTGTATATTTAATT
 ACGAATATTAAAGATGATAACGGTATCGCTGCTGTTAAGGTACCGGTTTG
 GACTGAACAGGAGGCGCAAGATGATATTAATGGTATACAGCTGTAACATA
 CTGGGGATGGCAACTACAAAGTAGCTGTATCATTTGCTGACCATAGAAT
 GAGAAGGGTCTTTATAAATTTCAATTTATACTACCAAGAAGCTAGTGGGAC
 ACTTGTAGGTGTAAACAGGAATAAAGTGACAGTAGCTGGAACATAATCTTT
 CTCAAGAACCTATTGAAAAATGGTTTACCAAGAGCTGGTGTTTATAATATT
 ATCGGAAGTACTGAAGTAAAAAATGAAGCTAAAAATATCAAGTCAGACCCA
 ATTTACTTTAGAAAAAGGTGACAAAAATAAATTATGATCAAGTATTGACAG
 CAGATGGTTTACCAAGTGGATTTCTTACAAATCTTATAGTGGTGTTCGTGCG
 TATATTTCTGTGAAAAAGCTAACTACAAGTAGTAAAAAGCGAAAGATGA
 GGCGACTAAACCGACTAGTTATCCCAACTTACCTAAACAGGTACCTATA
 CATTTACTAAAACCTGTAGATGTGAAAAGTCAACCTAAAGTATCAAGTCCA
 GTGGAAATTTAATTTTCAAAAGGGTGAAAAATACATTATGATCAAGTGT
 AGTAGTAGATGGTATCAGTGGATTTCATACAAAGATTATTCCGGTATTC
 GTCGTATATTGAAATT

SEQ ID NO. 8907

STRAIN COH1

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTTACTCTCT
 ACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTCTATAA
 TGGTCACAAGTCCGTGTTTTCGCGATCAAACTACATCGGTTCAAGTTAAT
 AATCAGACAGGCACTAGTGTGGATGCTAATAATCTTCCAATGAGACAAG
 TGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCGTCTGATA
 AAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCCTTTA
 GTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAGGGAATTA
 TGTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAAATCAGCCC
 CAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTCTATGACCAAGTA
 TTTAATAAAGATAATGTTAAATGGATTTCATATAAGTCTTTTGGTGGCGT
 ACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTTCAGAGA
 CTAAGACACCTACTCTGTAAACAAATTCAGGAAGCAATAATCAAGAGAAA
 ATAGCAACGCAAGGAAATTTATACATTTTACATAAAGTAGAAGTAaAAAA
 TGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGAGACA
 GAATTTTTTACGACCAATACTAATCTATTGAAGGAAATCAGTGGTTATCT
 TATAAATCATTTCAATGGTGTTCGTGCTTTTGTCTGCTAGGTAAAGCATC
 TTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCTCAACCACAAG
 CCCGTTTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAACTACA
 GGTTTTGTATTTTAAATTCGAATATTAAAGATGATAACGGTATCGCTGC
 TGTTAAGGTACCGGTTTGGACTGAACAAGGAGGCAAGATGATATTAAAT
 GGTATACAGCTGTAACTACTGGGGATGGCAACTACAAAGTAGCTGTATCA
 TTTGCTGACCATAGAATGAGAAGGGTCTTTATAAATTTCAATTTATACTA
 CCAAGAAGCTAGTGGGACACTTGTAGGTGAACAGGAATAAAGTGACAG
 TAGCTGGAATAATCTTCTCAAGAACCTATTGAAAAATGGTTTACCAAG
 ACTGGTGTTTATAAATATATCGGAAGTACTGAAGTAAAAAATGAAGCTAA
 AATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAATAAATT
 ATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTCTTACAAATCT
 TATAGTGGTGTTCGTGCTATATTCTGTGAAAAAGCTAACTACAAGTAG
 TGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACTTAC
 CTAAAAACAGGTACCTATACATTTACTAAAACCTGTAGATGTGAAAAGTCAA
 CCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAAGGGTGAAAAAT
 ACATTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTTCATACA
 AGAGTTATTCCGGTATTTCGTGCTATATTGAAATT

SEQ ID NO. 8908

STRAIN M781

Table 89: Comparative Sequences relating to SAG1350

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTT
 ACTCTCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCA
 TTCATAATGGTCAACAAGTCTGTCTTTTGGGATCAAACCTACATCGGTTCA
 AGTTAATAATCAGACAGGCACTAGTGTGGATGCTAATAATCTTCCAATG
 AGACAAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCG
 TCTGATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTAC
 TCCTTTAGTAGAGACAAAGCCAATGGTGGAAAAACATTACCTGAACAG
 GGAATTATGTTTATAGCAAAAGAAACCGAGGTGAAAAATACACCTTCAAAA
 TCAGCCCCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTCTATGA
 CCAAGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTG
 GTGGCGTACGTGATACGACGCTATTGAGTCACTAGATCCATCAGGAGGT
 TCAGAGACTAAAGCACCTACTCTGTAAACAAATTCAGGAAGCAATAATCA
 AGAGAAAATAGCAACGCAAGGAAATATACATTTTCACTATAAGTAGAAG
 TAAAAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAA
 GGAGACAGAAATTTTACGACCAAACTACTAATTTGAAGGAAATCAGTG
 GTTATCTTATAAATCATTTCAATGGTGTTCGTCTTTTGTCTGCTAGGTA
 AAGCATCTTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAA
 CCACAAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAAC
 AACTACAGGTTTGTATATTTAATTACGAATATTAAAGATGATAACGGTA
 TCGCTGCTGTAAAGTACCGGTTTGGACTGAACAGGAGGGCAAGATGAT
 ATTAATGGTATACAGCTGTAACTACTGGGGATGGCACTACAAAGTAGC
 TGTATCATTTGCTGACCATAGAATGAGAAGGGTCTTTATAATATTCTATT
 TATACACCAAGAAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAA
 GTGACAGTAGCTGGAACATAATCTTCTCAAGAACCTATTGAAATGGTTT
 ACCAAAGACTGGTGTATATAATATTATCGGAAGTACTGAAGTAAAAATG
 AAGCTAAAATATCAAGTCAAGCCAAATTTACTTTAGAAAAAGGTGACAAA
 ATAAATTTAGTCAAGTATTTGACAGCAGATGGTTACCAAGTGGATTTCTTA
 CAAATCTTATAGTGGTGTTCGTGCTATATCTCTGTGAAAAAGCTAACTA
 CAGTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCC
 AACTTACCTAAAACAGGTACCTATACATTTTACTAAAACCTGATAGTGTGAA
 AAGTCAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTG
 AAAAAATACATTATGATCAAGTGTAGTAGTAGATGGTCACTAGTGGATT
 TCATACAAGAGTTATTCGGGTATTCGTGCTATATTGAAATT

SEQ ID NO. 8909

STRAIN CJB110

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTTACTCTC
 TACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTATA
 ATGGTCAACAAGTCTGTCTTTTGGGATCAAACCTACATCGGTTCAAGTTAA
 TAATCAGACAGGCACTAGTGTGGATGCTAATAATCTTCCAATGAGACAA
 GTGCGTCAAGTGTGATTACTTCCAATATGATAGTGTCAAGCGTCTGAT
 AAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCTTT
 AGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAAGGGAAT
 ATGTTTATAGCAAAAGAACCGAGGTGAAAAATACACCTTCAAAATCAGCC
 CCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTCTATGACCAAGT
 ATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTGTGGCG
 TACGTGATACGACGCTATTGAGTCACTAGATCCATCAGGAGGTTTCAGAG
 ACTAAAGCACCTACTCTGTAAACAAATTCAGGAAGCAATAATCAAGAGAA
 AATAGCAACGCAAGGAAATATACATTTTCACTAAAGTAGAAGTAAAAA
 ATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGAGAC
 AGAATTTTACGACCAAAATATACTAATTTGAAGGAAATCAGTGGTTATC
 TTATAAATCATTTCAATGGTGTTCGTCTTTTGTCTGCTAGGTAAAGCAT
 CTTCAAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCTCAACCCAA
 GCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACCACTAC
 AGGTTTGTATATTTAATTACGAATATTAAAGATGATAACGGTATCGCTG
 CTGTTAAGGTACCGGTTTGGACTGAACAGGAGGGCAAGATGATATTA
 TGGTATACAGCTGTAACCTACTGGGATGGCACTACAAAGTAGCTGTATC
 ATTTGCTGACCATAGAATGAGAAGGGTCTTTATAATATTCAATTTACT
 ACCAAGAAGCTAGTGGGACACTTGTAGGTGTACAGGAACATAAGTGACA
 GTAGCTGGAACATAATCTTCTCAAGAACCTATTGAAATGGTTAGCAAA
 GACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAATGAAGCTA
 AAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAATAAAT
 TATGATCAAGTATTGACAGCAGATGGTTACCAAGTGGATTCTTACAAATC
 TTATAGTGGTGTTCGTGCTATATTCTGTGAAAAAGCTAACTACAAAGTA
 GTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACTTA
 CCTAAACAGGTACCTATACATTTACTAAAACCTGTAGATGTGAAGAGTCA
 ACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAAAAAA
 TACATTATGATCAAGTGTAGTAGTAGATGGTCACTAGTGGATTTCATAC
 AAGATTATTCGGGTATTCGTGCTATATTGAAATT

SEQ ID NO. 8910

STRAIN 1169NT

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTTACTC
 TCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTCA
 TAATGGTCAACAAGTCTGTCTTTTGGGATCAAACCTACATCGGTTCAAGTT
 AATAATCAGACAGGCACTAGTGTGGATGCTAATAATCTTCCAATGAGAC
 AAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCGTCTG
 ATAAAGTTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTCT
 TTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAAGGAA
 TTATGTTTATAGCAAAAGAAACCGAGGTGAAAAATACACCTTCAAAATCAG
 CCCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTCTATGACCAA
 GTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTGGTGG
 CGTACGTGATACGACGCTATTGAGTCACTAGATCCATCAGGAGGTTTCAG

Table 89: Comparative Sequences relating to SAG1350

AGACTAAAGCACCTACTCCTGTAAACAAATTCAGGAAGCAATAATCAAGAG
 AAAATAGCAACGCAAGGAAATTTATACATTTTCACATAAAGTAGAAGTAAA
 AAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGAG
 ACAGAATTTTACGACCAATATACTAATTTGAAGGAAATCAGTGGTTA
 TCTTATAAATCAATCAATGGTGTTCGTGTTTTGTTTTGCTAGGTAAAGC
 ATCTTCAGTAGAAAAAAGTGAAGATAAAGAAAAAGTGTCTCTCAACCAC
 AAGCCCGTATTACTAAACTGGTAGACTGACTATTTCTAACGAAACCACT
 ACAGGTTTTGATATTTAATTAACGAATATTAAGATGATAACGGTATCGC
 TGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGCAAGATGATATTA
 AATGGTATACAGCTGTAACACTGGGGATGGCAACTACAAAGTAGCTGTA
 TCATTTGCTGACCATAGAATGAGAAGGGTCTTTATAATATTCATTTATA
 CTACCAAGAGCTAGTGGGACACTTGTAGGTGTAACAGGAATAAAGTGA
 CAGTAGCTGGAaCTAATTCCTCTCAAGAACCTATTGAAAAAGGTTTAGCA
 AAGACTGGTGTATTATAATATTCGGAAGTACTGAAGTAAAAATGAAGC
 TAAATATCAAGTCAGACCCAATTTACTTTAGAAAAGGTGACAAATAA
 ATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTCTTACAAA
 TCTTATAGTGGTGTTCGTGCTATATTCTGTGAAAAAGCTAACTACAAG
 TAGTGA AAAAGCGAAGATGAGGCGACTAAACCGACTAGTTATCCCACT
 TACCTAAAACAGGTACCTATACATTTACTAAAAGTGTAGATGTGAAAAGT
 CAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAAAA
 AATACATTATGATCAAGTGTAGTAGTAGTGGTCATCAGTGGATTTCAT
 ACAAGAGTTATTCGGTATTTCGTGCTATATTGAAATT

SEQ ID NO. 8911

STRAIN JM9130013

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACT
 CTCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTC
 ATAATGGTCACAAGTCTCTGTTTTGCGGATCAAACATACGCGTTCAAGT
 TAATAATCAGACAGGCACCTAGTGTGGATGCTAATAATTTCTTCAATGAGA
 CAAGTGCCTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCT
 GATAAAGTTGTAATAGTCAAAATACGGCAACAAAGGACATTACTACTCC
 TTTAGTAGAGACAAAGCCAATGGTGGAAAAACATTTACCTGAACAAGGGA
 ATTATGTTTATAGCAAGAAACCGAGGTGAAAAATACACCTTCAAATCA
 GCCCAGTAGCTTTCTATGCAAGAAAGGTGATAAAGTTTTCTATGACCA
 AGTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTGTG
 GCGTACGTCGATACGAGCTATTGAGTCACTAGATCCATCAGGAGGTTCA
 GAGACTAAAGCACCTACTCTCTGTAACAAATTCAGGAAGCAATAATCAAGA
 GAAATAGCAACGCAAGGAAATTTATACATTTTTCACATAAAGTAGAAGTAA
 AAAATGAAGCTAAGGTAGCGAGTCCAACTCAATTTACATTGGACAAAGGA
 GACAGAATTTTTACGACCAAAATACTAACTATTGAAGGAATCAGTGGTT
 ATCTTATAAATCATTCATGGTGTTCGTGTTTTGTTTTGCTAGGTAAAG
 CATCTTCAGTAGAAAAAAGTGAAGATAAAGAAAAAGTGTCTCCTCAACCA
 CAAGCCCGTATTACTAAAAGTGGTAGACTGACTATTTATAACGAAACCAAC
 TACAGGTTTTGATATTTAATTACGAATATAAAGATGATAACGGTATCG
 TCGCTTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATT
 AAATGGTATACAGCTGTAACCTACTGGGGATGGCAACTACAAAGTAGCTGT
 ATCATTTGCTGACCATAGAATGAGAAGGGTCTTTATAATATTCATTTAT
 ACTACCAAGAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAGTG
 ACAGTAGCTGGAACTAATTCCTCTCAAGAACCTATTGAAAATGGTTTAGC
 AAAGACTGGTGTATTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAG
 CTAAATATCAAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAAATA
 AATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTCTTTACAA
 ATCTTATAGTGGTGTTCGTGCTATATTCTCTGAAAAAGCTAACTACAA
 GTAGTGAAAAAGCGAAGATGAGGCGACTAAACCGACTAGTTATCCCAAC
 TTACCTAAAACAGGTACCTATACATTTACTAAAAGTGTAGATGTGAAGAG
 TCAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTGAAA
 AAATACATTATGATCAAGTGTAGTAGTAGTGGTCATCAGTGGATTTCAT
 TACAAGAGTTATTCCGGTATTTCGTGCTATATTGAAATT

PRETTY of: /biotmp/msa255059.2{*} February 11, 2003 08:41 ..

	1			50
msa255059.2{91_M732}	-----	--CAAGTAAA	TGATACTAAG	CAATCTTACT CTCTACGTAA
msa255059.2{91_M781}	----	AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_COH1}	----	AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_18RS21}	----	AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_2603}	atg	AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_1169NT}	----	AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_090}	----	AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_A909}	----	AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_CJB110}	----	AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_H36B}	----	AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
msa255059.2{91_JM9130013}	----	AAAAAAG	GACAAGTAAA	TGATACTAAG CAATCTTACT CTCTACGTAA
Consensus	*****	*****	*****	*****

	51			100
msa255059.2{91_M732}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC ATAATGGTCA
msa255059.2{91_M781}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC ATAATGGTCA
msa255059.2{91_COH1}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC ATAATGGTCA
msa255059.2{91_18RS21}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC ATAATGGTCA
msa255059.2{91_2603}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC ATAATGGTCA
msa255059.2{91_1169NT}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC ATAATGGTCA

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_090}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_A909}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_CJB110}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_H36B}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_JM9130013}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_M781}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_COH1}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_18RS21}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_2603}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_1169NT}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_090}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_A909}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_CJB110}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_H36B}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_JM9130013}	CAAGTCCTGT	TTTTGCGGAT	CAAACTACAT	CGGTTCAAGT	TAATAATCAG
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_M781}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_COH1}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_18RS21}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_2603}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_1169NT}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_090}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_A909}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_CJB110}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_H36B}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_JM9130013}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_M781}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_COH1}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_18RS21}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_2603}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_1169NT}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_090}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_A909}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_CJB110}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_H36B}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_JM9130013}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_M781}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_COH1}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_18RS21}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_2603}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_1169NT}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_090}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_A909}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_CJB110}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_H36B}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_JM9130013}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_M781}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_COH1}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_18RS21}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_2603}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_1169NT}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_090}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_A909}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_CJB110}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_H36B}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_JM9130013}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_M781}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_COH1}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_18RS21}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_2603}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_1169NT}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_090}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_A909}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_CJB110}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_H36B}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_JM9130013}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
Consensus	*****	*****	*****	*****	*****
401	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_M732}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_M781}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_COH1}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_18RS21}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_2603}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_1169NT}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_090}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_A909}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_CJB110}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_H36B}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_JM9130013}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
Consensus	*****	*****	*****	*****	*****
451	AAAGATAATG	TgAAATGGAT	TTCAATATAAG	TCCTTTgGTG	GCGTACGTCG
msa255059.2{91_M732}	AAAGATAATG	TgAAATGGAT	TTCAATATAAG	TCCTTTgGTG	GCGTACGTCG
msa255059.2{91_M781}	AAAGATAATG	TgAAATGGAT	TTCAATATAAG	TCCTTTgGTG	GCGTACGTCG
msa255059.2{91_COH1}	AAAGATAATG	TgAAATGGAT	TTCAATATAAG	TCCTTTgGTG	GCGTACGTCG
msa255059.2{91_18RS21}	AAAGATAATG	TgAAATGGAT	TTCAATATAAG	TCCTTTgGTG	GCGTACGTCG
msa255059.2{91_2603}	AAAGATAATG	TgAAATGGAT	TTCAATATAAG	TCCTTTgGTG	GCGTACGTCG
msa255059.2{91_1169NT}	AAAGATAATG	TgAAATGGAT	TTCAATATAAG	TCCTTTgGTG	GCGTACGTCG
msa255059.2{91_090}	AAAGATAATG	TgAAATGGAT	TTCAATATAAG	TCCTTTgGTG	GCGTACGTCG
msa255059.2{91_A909}	AAAGATAATG	TgAAATGGAT	TTCAATATAAG	TCCTTTgGTG	GCGTACGTCG
msa255059.2{91_CJB110}	AAAGATAATG	TgAAATGGAT	TTCAATATAAG	TCCTTTgGTG	GCGTACGTCG
msa255059.2{91_H36B}	AAAGATAATG	TgAAATGGAT	TTCAATATAAG	TCCTTTgGTG	GCGTACGTCG
msa255059.2{91_JM9130013}	AAAGATAATG	TgAAATGGAT	TTCAATATAAG	TCCTTTgGTG	GCGTACGTCG
Consensus	*****	*..*****	*****	*****_***	*****
501	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_M732}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_M781}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_COH1}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_18RS21}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_2603}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_1169NT}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_090}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_A909}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_CJB110}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_H36B}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_JM9130013}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
Consensus	*****	*****	*****	*****	*****
551	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_M732}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_M781}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_COH1}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_18RS21}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_2603}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_1169NT}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_090}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_A909}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_CJB110}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_H36B}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
msa255059.2{91_JM9130013}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAAATAGCA
Consensus	*****	*****	*****	*****	*****
601	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_M732}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_M781}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_COH1}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_18RS21}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_2603}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_1169NT}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_090}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_A909}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_CJB110}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_H36B}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_JM9130013}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
Consensus	*****	*****	*****	*****	*****
651	TAAGGTAGCG	AGTCCAATC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_M732}	TAAGGTAGCG	AGTCCAATC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_M781}	TAAGGTAGCG	AGTCCAATC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_COH1}	TAAGGTAGCG	AGTCCAATC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_18RS21}	TAAGGTAGCG	AGTCCAATC	AATTTACATT	GGACAAAGGA	GACAGAATTT

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_2603}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_1169NT}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_090}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_A909}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_CJB110}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_H36B}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_JM9130013}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_M781}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_COH1}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_18RS21}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_2603}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_1169NT}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_090}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_A909}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_CJB110}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_H36B}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_JM9130013}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_M781}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_COH1}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_18RS21}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_2603}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_1169NT}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_090}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_A909}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_CJB110}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_H36B}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_JM9130013}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	AGAAAAA	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_M781}	AGAAAAA	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_COH1}	AGAAAAA	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_18RS21}	AGAAAAA	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_2603}	AGAAAAA	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_1169NT}	AGAAAAA	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_090}	AGAAAAA	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_A909}	AGAAAAA	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_CJB110}	AGAAAAA	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_H36B}	AGAAAAA	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_JM9130013}	AGAAAAA	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCCGTA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_M781}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_COH1}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_18RS21}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_2603}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_1169NT}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_090}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_A909}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_CJB110}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_H36B}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_JM9130013}	TTACTAAAAC	TGGTAGACTG	ACTATTTCtA	ACGAAACAAC	TACAGGTTTT
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_M781}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_COH1}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_18RS21}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_2603}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_1169NT}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_090}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_A909}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_CJB110}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_H36B}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_JM9130013}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_M781}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_COH1}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_18RS21}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_2603}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_1169NT}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_090}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_A909}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_CJB110}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_H36B}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_JM9130013}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_M781}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_COH1}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_18RS21}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_2603}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_1169NT}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_090}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_A909}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_CJB110}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_H36B}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_JM9130013}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_M781}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_COH1}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_18RS21}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_2603}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_1169NT}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_090}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_A909}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_CJB110}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_H36B}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
msa255059.2{91_JM9130013}	GACCATAAGA	ATGAGAAGGG	TCITTTATAAT	ATTCAATTTAT	ACTACCAAGA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_M781}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_COH1}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_18RS21}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_2603}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_1169NT}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_090}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_A909}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_CJB110}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_H36B}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_JM9130013}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_M781}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_COH1}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_18RS21}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_2603}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_1169NT}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_090}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_A909}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_CJB110}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_H36B}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_JM9130013}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_M781}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_COH1}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_18RS21}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_2603}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_1169NT}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_090}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_A909}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_CJB110}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_H36B}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_JM9130013}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_M781}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC

msa255059.2{91_COH1}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_18RS21}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_2603}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_1169NT}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_A909}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_CJB110}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_H36B}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_JM9130013}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	1301	AGCAGATGGT	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_M781}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_COH1}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_18RS21}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_2603}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_1169NT}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_A909}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_CJB110}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_H36B}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_JM9130013}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGG	TTTCTTACAA	ATCTTATAGT
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	1351	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAAA
msa255059.2{91_M781}	GGTGTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAAA
msa255059.2{91_COH1}	GGTGTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAAA
msa255059.2{91_18RS21}	GGTGTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAAA
msa255059.2{91_2603}	GGTGTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAAA
msa255059.2{91_1169NT}	GGTGTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAAA
msa255059.2{91_A909}	GGTGTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAAA
msa255059.2{91_CJB110}	GGTGTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAAA
msa255059.2{91_H36B}	GGTGTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAAA
msa255059.2{91_JM9130013}	GGTGTTCGTC	GCTATATTCC	TGTGAAAAG	CTAACTACAA	GTAGTGAAAA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	1401	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_M781}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_COH1}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_18RS21}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_2603}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_1169NT}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_A909}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_CJB110}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_H36B}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_JM9130013}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	1451	TACATTTACT	AAAACCTGAT	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_M781}	CAGGTACCTA	TACATTTACT	AAAACCTGAT	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_COH1}	CAGGTACCTA	TACATTTACT	AAAACCTGAT	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_18RS21}	CAGGTACCTA	TACATTTACT	AAAACCTGAT	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_2603}	CAGGTACCTA	TACATTTACT	AAAACCTGAT	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_1169NT}	CAGGTACCTA	TACATTTACT	AAAACCTGAT	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_A909}	CAGGTACCTA	TACATTTACT	AAAACCTGAT	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_CJB110}	CAGGTACCTA	TACATTTACT	AAAACCTGAT	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_H36B}	CAGGTACCTA	TACATTTACT	AAAACCTGAT	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_JM9130013}	CAGGTACCTA	TACATTTACT	AAAACCTGAT	ATGTGAAaAG	TCAACCTAAA
Consensus	*****	*****	*****	*****	*****
msa255059.2{91_M732}	1501	CAGTGAaATT	TAATTTTCAA	AAGGGTGAAA	AAATACATTA
msa255059.2{91_M781}	GTATCAAGTC	CAGTGAaATT	TAATTTTCAA		

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_M781}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_COH1}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_18RS21}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_2603}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_1169NT}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_090}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_A909}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_CJB110}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_H36B}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_JM9130013}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
Consensus	*****	*****	*****	*****	*****

	1601		1629
msa255059.2{91_M732}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_M781}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_COH1}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_18RS21}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_2603}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_1169NT}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_090}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_A909}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_CJB110}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_H36B}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_JM9130013}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
Consensus	*****	*****	*****

SEQ ID NO. 8912

STRAIN 2603 frame: 1

MKKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSPPVFADQTTSVQVNNQTGTSVDANNSS
 SNETSASSVITSNNDSVQASDKVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYYSKE
 TEVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFQGVRRYAAIESLDPGGSS
 ETKAPTPTVNSGNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFDYDQILTI
 IEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFADHKNEKGLYNI
 HLYYQEAAGTLLVGVTGKVTGAGTNSQEPINGLAKTGNYNIIGSTEVEKNEAKISSQTQ
 FTLEKGDKNINYDQVLADGYQWISYKSYSGVRRYIPVKKLTTSSSEKAKDEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVDGHWISYKSYSGIRRYI
 EI

SEQ ID NO. 8913

STRAIN 090 frame: 1

KKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSPPVFADQTTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYYSKET
 EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFQGVRRYAAIESLDPGGSE
 TKAPTPTVNSGNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFDYDQILTI
 IEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFADHKNEKGLYNI
 HLYYQEAAGTLLVGVTGKVTGAGTNSQEPINGLAKTGNYNIIGSTEVEKNEAKISSQTQ
 FTLEKGDKNINYDQVLADGYQWISYKSYSGVRRYIPVKKLTTSSSEKAKDEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVDGHWISYKSYSGIRRYI
 EI

SEQ ID NO. 8914

STRAIN A909 frame: 1

KKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSPPVFADQTTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYYSKET
 EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFQGVRRYAAIESLDPGGSE
 TKAPTPTVNSGNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFDYDQILTI
 IEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFADHKNEKGLYNI
 HLYYQEAAGTLLVGVTGKVTGAGTNSQEPINGLAKTGNYNIIGSTEVEKNEAKISSQTQ
 FTLEKGDKNINYDQVLADGYQWISYKSYSGVRRYIPVKKLTTSSSEKAKDEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVDGHWISYKSYSGIRRYI
 EI

SEQ ID NO. 8915

STRAIN H36B frame: 1

KKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSPPVFADQTTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYYSKET
 EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFQGVRRYAAIESLDPGGSE
 TKAPTPTVNSGNNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFDYDQILTI
 IEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFADHKNEKGLYNI
 HLYYQEAAGTLLVGVTGKVTGAGTNSQEPINGLAKTGNYNIIGSTEVEKNEAKISSQTQ
 FTLEKGDKNINYDQVLADGYQWISYKSYSGVRRYIPVKKLTTSSSEKAKDEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVDGHWISYKSYSGIRRYI
 EI

SEQ ID NO. 8916

STRAIN 18RS21 frame: 1

KKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSPPVFADQTTSVQVNNQTGTSVDANNSS
 NETSASSVITSNNDSVQASDKVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYYSKET

Table 89: Comparative Sequences relating to SAG1350

EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFVGGVRRYAAIESLDPSSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSSHKEVEKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIDKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNKYKAVSFADHNEKGLYNI
HLYYQEASGTLVGVTGKVTVAGTNSSQEPINENGLAKTGNYNIIGSTEVEKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8917

STRAIN M732 frame: 1

QVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSSNET
SASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKETEVK
NTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFVGGVRRYAAIESLDPSSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSSHKEVEKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIDKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNKYKAVSFADHNEKGLYNIHLY
YQEASGTLVGVTGKVTVAGTNSSQEPINENGLPKTGNYNIIGSTEVEKNEAKISSQTQFTL
EKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
GTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYIEI

SEQ ID NO. 8918

STRAIN COH1 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFVGGVRRYAAIESLDPSSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSSHKEVEKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIDKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNKYKAVSFADHNEKGLYNIHLY
YQEASGTLVGVTGKVTVAGTNSSQEPINENGLPKTGNYNIIGSTEVEKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8919

STRAIN M781 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFVGGVRRYAAIESLDPSSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSSHKEVEKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIDKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNKYKAVSFADHNEKGLYNIHLY
YQEASGTLVGVTGKVTVAGTNSSQEPINENGLPKTGNYNIIGSTEVEKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8920

STRAIN CJB110 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFVGGVRRYAAIESLDPSSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSSHKEVEKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIDKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNKYKAVSFADHNEKGLYNIHLY
YQEASGTLVGVTGKVTVAGTNSSQEPINENGLAKTGNYNIIGSTEVEKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8921

STRAIN 1169NT frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFVGGVRRYAAIESLDPSSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSSHKEVEKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIDKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNKYKAVSFADHNEKGLYNIHLY
YQEASGTLVGVTGKVTVAGTNSSQEPINENGLAKTGNYNIIGSTEVEKNEAKISSQTQ
FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLITSSEKAKDEATKPTSYPNL
PKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8922

STRAIN JM9130013 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNQTGTSVDANNSS
NETSASSVITSNNDSVQASDKVNSQNTATKDITPLVETKPMVEKTLPEQGNVYVSKET
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFVGGVRRYAAIESLDPSSGGSE
TKAPTPTVNTSGSNNOEKIATQGNVTFSSHKEVEKNEAKVASPTQFTLDKGDRIFYDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIDKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNKYKAVSFADHNEKGLYNIHLY
YQEASGTLVGVTGKVTVAGTNSSQEPINENGLAKTGNYNIIGSTEVEKNEAKISSQTQ

Table 89: Comparative Sequences relating to SAG1350

FTLEKGDKINYDQVLTDGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYYTFTKTVDKVSQPKVSSPFVEFNFQKGEKIHVDQVLVDGHWISYKSYSGIRRYI
EI

PRETTY of: /biotmp/msa255178.2{*} February 11, 2003 08:51 ..

	1				50
msa255178.2{91_090}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_18RS21}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_2603}	mkkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_A909}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_CJB110}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_H36B}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_JM9130013}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_COH1}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_M781}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_M732}	----QVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
msa255178.2{91_1169NT}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSVPFAD	QTTSVQVNNQ
Consensus	*****	*****	*****	*****	*****
	51				100
msa255178.2{91_090}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_18RS21}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_2603}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_A909}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_CJB110}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_H36B}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_JM9130013}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_COH1}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_M781}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_M732}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
msa255178.2{91_1169NT}	TGTSVDaNNs	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPPLVE
Consensus	*****	*****	*****	*****	*****
	101				150
msa255178.2{91_090}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_18RS21}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_2603}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_A909}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_CJB110}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_H36B}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_JM9130013}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_COH1}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_M781}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_M732}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
msa255178.2{91_1169NT}	TKPMVEKTLp	EQGNYVYSKE	TEVKNTPSKS	APVAFYAKKG	DKVFYDQVFN
Consensus	*****	*****	*****	*****	*****
	151				200
msa255178.2{91_090}	KDNVKWISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_18RS21}	KDNVKWISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_2603}	KDNVKWISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_A909}	KDNVKWISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_CJB110}	KDNVKWISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_H36B}	KDNVKWISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_JM9130013}	KDNVKWISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_COH1}	KDNVKWISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_M781}	KDNVKWISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_M732}	KDNVKWISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
msa255178.2{91_1169NT}	KDNVKWISYK	SfCGVRRYAA	IESLDPSGGS	ETKAPTPTVN	SGSNNQEKIA
Consensus	*****	*****	*****	*****	*****
	201				250
msa255178.2{91_090}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_18RS21}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_2603}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_A909}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_CJB110}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_H36B}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_JM9130013}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_COH1}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_M781}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_M732}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
msa255178.2{91_1169NT}	TQGNyTFSHK	VEVKNEAKVA	SPTQFTLDKG	DRIFYDQILT	IEGNQWLSYK
Consensus	*****	*****	*****	*****	*****
	251				300
msa255178.2{91_090}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TiSNETTTGF
msa255178.2{91_18RS21}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TiSNETTTGF
msa255178.2{91_2603}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TiSNETTTGF
msa255178.2{91_A909}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TiSNETTTGF
msa255178.2{91_CJB110}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TiSNETTTGF

Table 89: Comparative Sequences relating to SAG1350

msa255178.2{91_H36B}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TIsNETTTGF
msa255178.2{91_JM9130013}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TIsNETTTGF
msa255178.2{91_COH1}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TIsNETTTGF
msa255178.2{91_M781}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TIsNETTTGF
msa255178.2{91_M732}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TIsNETTTGF
msa255178.2{91_1169NT}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	TIsNETTTGF
Consensus	*****	*****	*****	*****	*_*-*****
msa255178.2{91_090}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNVKVAVSFA
msa255178.2{91_18RS21}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNVKVAVSFA
msa255178.2{91_2603}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNVKVAVSFA
msa255178.2{91_A909}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNVKVAVSFA
msa255178.2{91_CJB110}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNVKVAVSFA
msa255178.2{91_H36B}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNVKVAVSFA
msa255178.2{91_JM9130013}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNVKVAVSFA
msa255178.2{91_COH1}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNVKVAVSFA
msa255178.2{91_M781}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNVKVAVSFA
msa255178.2{91_M732}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNVKVAVSFA
msa255178.2{91_1169NT}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNVKVAVSFA
Consensus	*****	*****	*****	*****	*****
msa255178.2{91_090}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_18RS21}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_2603}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_A909}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_CJB110}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_H36B}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_JM9130013}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_COH1}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_M781}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_M732}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_1169NT}	DHKNEKGLYN	IHLYYQEASG	TLVGVTGTV	TVAGTNSSQE	PIENGLaKTG
Consensus	*****	*****	*****	*****	*****_***
msa255178.2{91_090}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_18RS21}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_2603}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_A909}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_CJB110}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_H36B}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_JM9130013}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_COH1}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_M781}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_M732}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_1169NT}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
Consensus	*****	*****	*****	*****	*****
msa255178.2{91_090}	GVRRIIPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_18RS21}	GVRRIIPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_2603}	GVRRIIPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_A909}	GVRRIIPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_CJB110}	GVRRIIPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_H36B}	GVRRIIPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_JM9130013}	GVRRIIPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_COH1}	GVRRIIPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_M781}	GVRRIIPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_M732}	GVRRIIPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_1169NT}	GVRRIIPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
Consensus	*****	*****	*****	*****	*****
msa255178.2{91_090}	VSSPVEFNQ	KGEKIHVDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_18RS21}	VSSPVEFNQ	KGEKIHVDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_2603}	VSSPVEFNQ	KGEKIHVDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_A909}	VSSPVEFNQ	KGEKIHVDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_CJB110}	VSSPVEFNQ	KGEKIHVDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_H36B}	VSSPVEFNQ	KGEKIHVDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_JM9130013}	VSSPVEFNQ	KGEKIHVDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_COH1}	VSSPVEFNQ	KGEKIHVDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_M781}	VSSPVEFNQ	KGEKIHVDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_M732}	VSSPVEFNQ	KGEKIHVDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_1169NT}	VSSPVEFNQ	KGEKIHVDQV	LVVDGHWIS	YKSYSGIRRY	IEI
Consensus	*****	*****	*****	*****	***

CLAIMS:

1. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is
5 encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of both GAS and *Streptococcus pneumoniae*.
2. The immunogenic composition of claim 1, wherein said GBS polypeptides are encoded by GBS polynucleotide sequences selected from GBS Subset 1.
3. An immunogenic composition comprising a combination of GBS polypeptides, said
10 combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of GAS.
4. The immunogenic composition of claim 3, wherein said GBS polypeptides are encoded by GBS polynucleotide sequences selected from GBS Subset 2.
- 15 5. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of *Streptococcus pneumoniae*.
6. The immunogenic composition of claim 5, wherein said GBS polypeptides are encoded
20 by GBS polynucleotide sequences selected from GBS Subset 3.
7. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS serotype polynucleotide sequence which is homologous to at least one other GBS serotype.
- 25 8. The immunogenic composition of claim 2, 4 or 6, wherein one or more of the GBS polypeptides are encoded by GBS serotype polynucleotide sequences which are homologous to at least one other GBS serotype.
9. An immunogenic composition comprising a fusion protein, wherein said fusion protein comprises a first polypeptide sequence which is encoded by a GBS serotype polynucleotide
30 which is conserved across one or more GBS serotypes.
10. A polynucleotide sequence, or a fragment comprising at least 10 contiguous polynucleotides, selected from the sequences set forth on Tables 13 – 31 and 40 – 89.
11. The polynucleotide fragment of claim 10, wherein said fragment is derived from a GBS serotype polynucleotide sequence and is homologous to at least one additional GBS serotype
35 polynucleotide sequence.

Figure 1

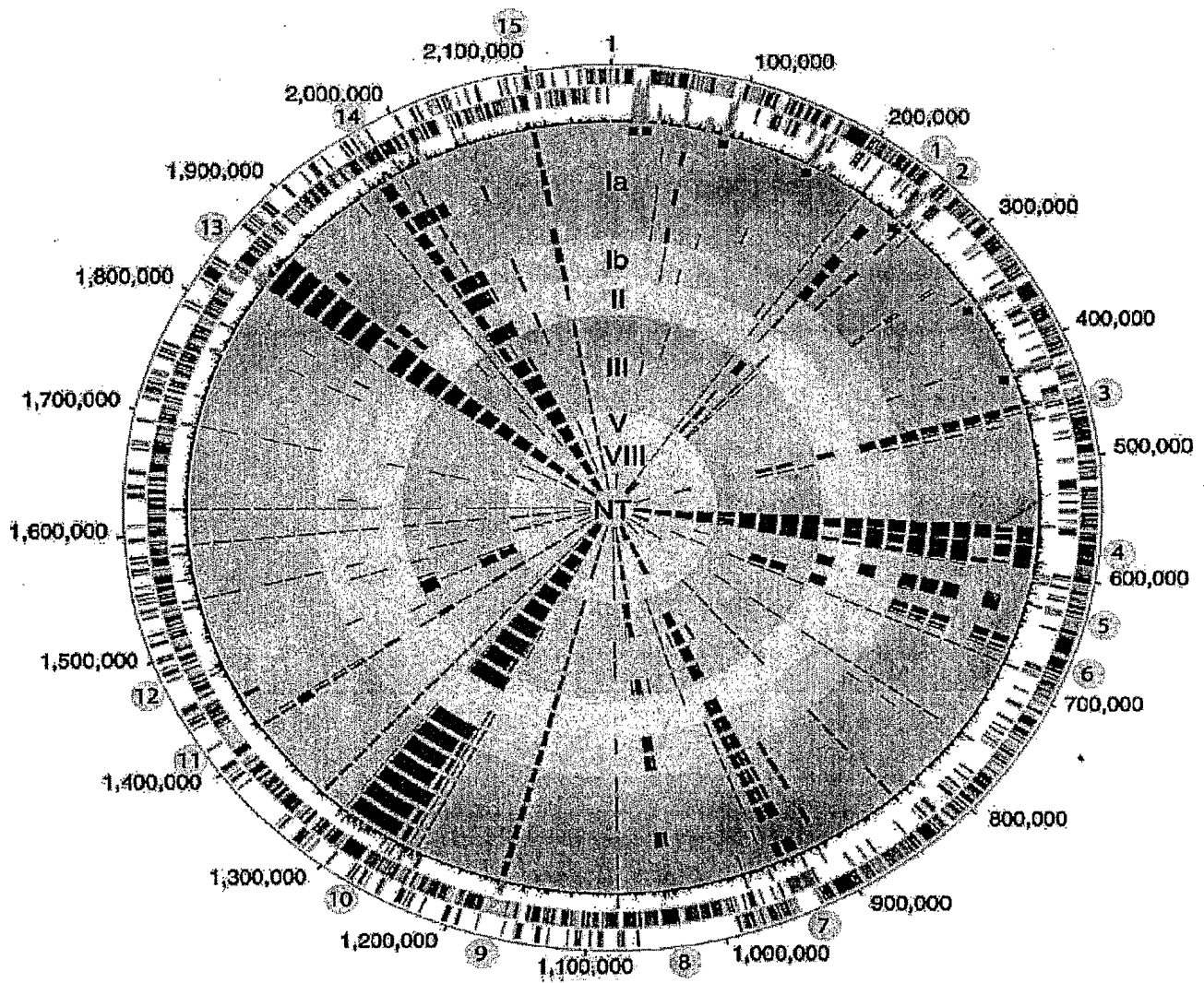


Figure 2

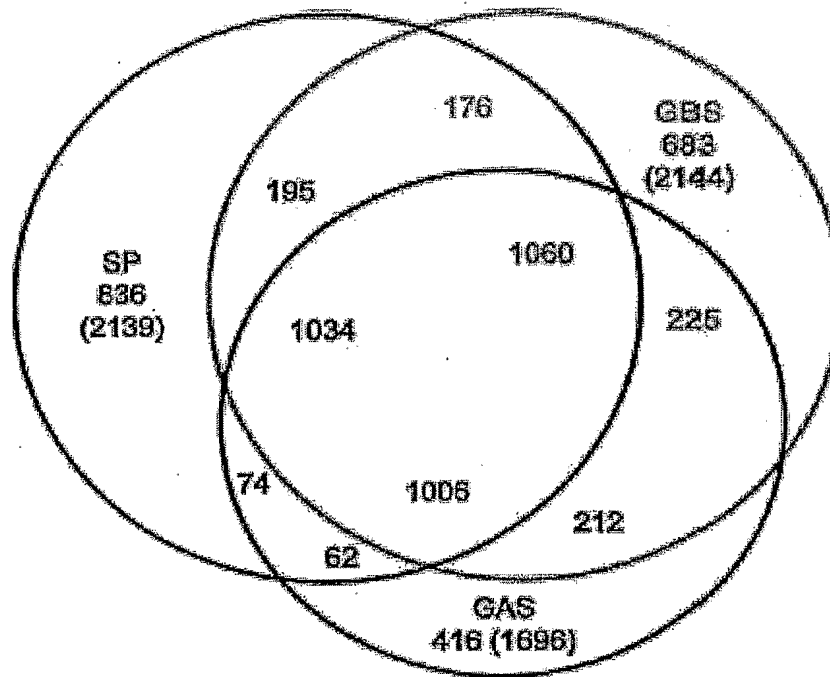
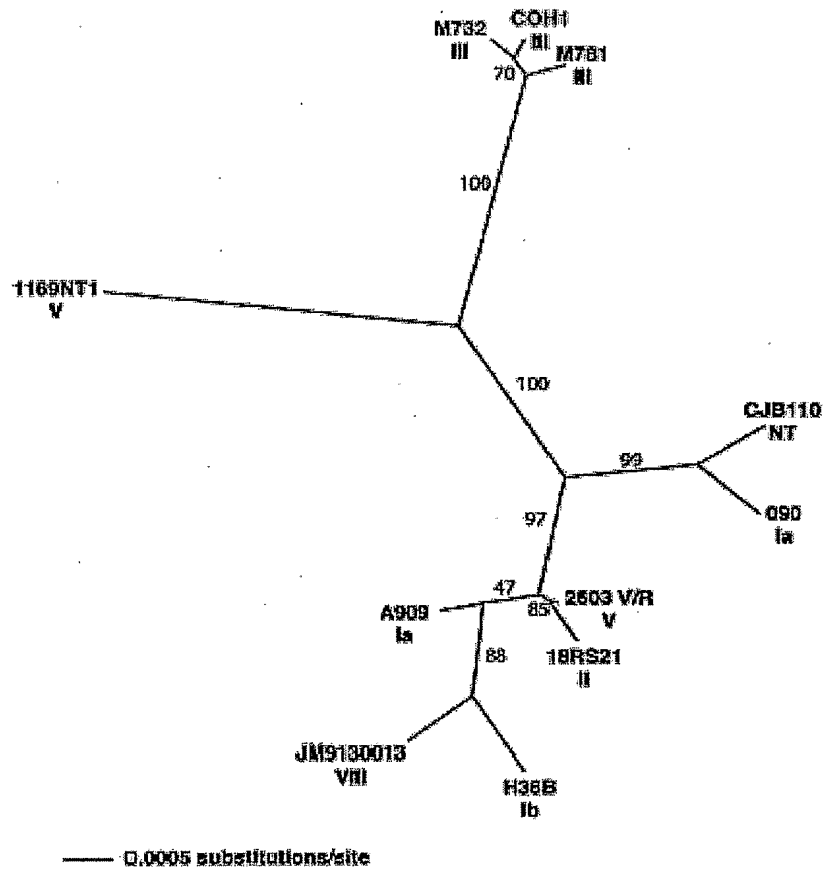


Figure 3



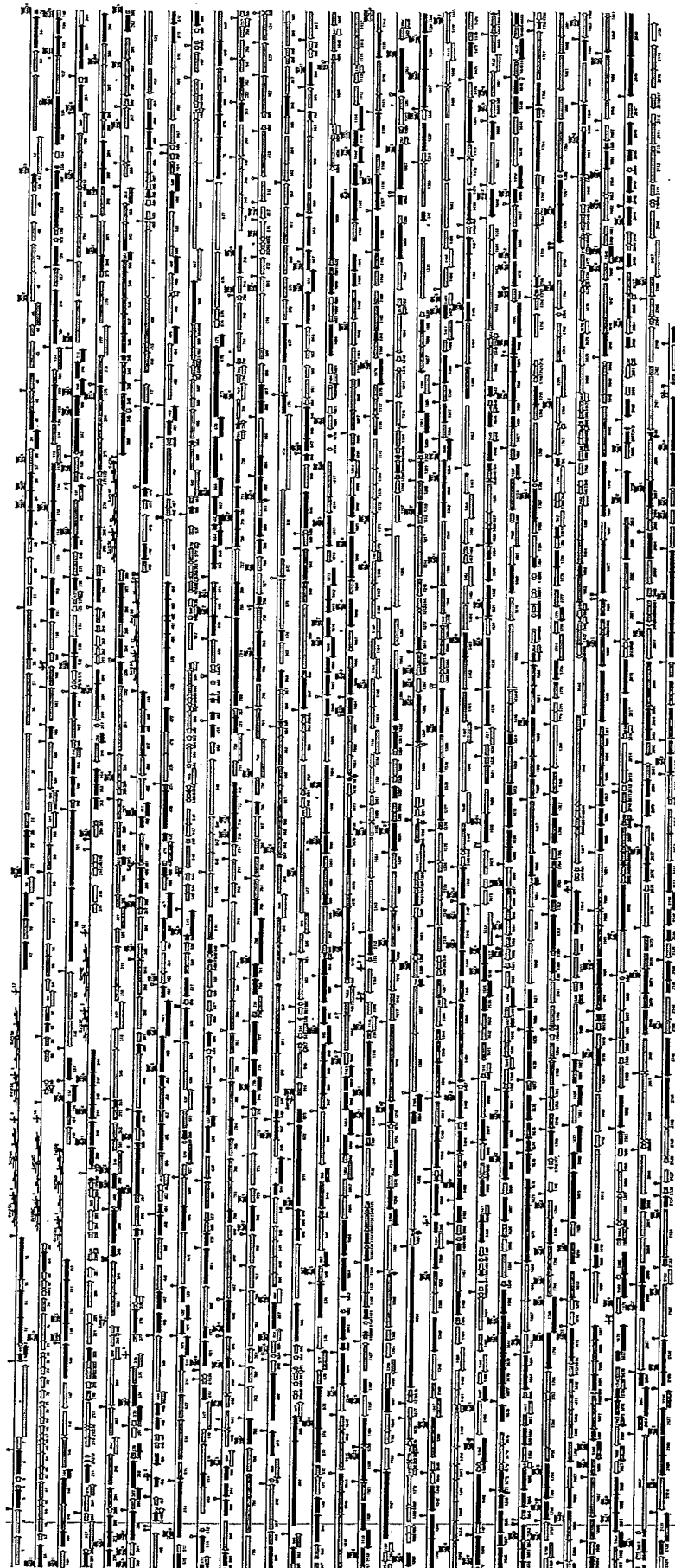


FIGURE 4

